

SEQUENCE LISTING

<110> ASAHI KASEI KABUSHIKI KAISHA

<120> NF- κ B Activating Gene

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<151> 2001-03-26

<150> JP 2001-254018

<151> 2001-08-24

<150> US 60/258, 315

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<150> US 60/278, 640

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<150> US 60/314, 385

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<160> 182

<170> PatentIn Ver. 2.0

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Ser Glu Tyr Pro Pro Phe Ser His Arg Tyr Gln Arg Phe Thr Asn Ser

Ala Gly Pro Pro Pro Pro Gly Phe Lys Ser Glu Phe Thr Gly Pro Gln

Asn Thr Gly His Gly Ala Thr Ser Gly Phe Gly Ser Ala Phe Thr Gly

Gln Gln Gly Tyr Glu Asn Ser Gly Pro Gly Phe Trp Thr Gly Leu Gly

Thr Gly Gly Ile Leu Gly Tyr Leu Phe Gly Ser Asn Arg Ala Ala Thr

Pro Phe Ser Asp Ser Trp Tyr Tyr Pro Ser Tyr Pro Pro Ser Tyr Pro

Met Ser Gly Leu Ile Thr Ile Val Val Leu Leu Gly

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Ile Ala Phe Val Val Tyr Lys Leu Phe Leu Ser Asp Gly Gln Tyr Ser

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cct cca ccg tac tct gag tat cct cca ttt tcc cac cgt tac cag aga 325

Pro Pro Pro Tyr Ser Glu Tyr Pro Pro Phe Ser His Arg Tyr Gln Arg

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Phe Thr Asn Ser Ala Gly Pro Pro Pro Pro Gly Phe Lys Ser Glu Phe

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aca gga cca cag aat act ggc cat ggt gca act tct ggt ttt ggc agt 421

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Ala Phe Thr Gly Gln Gln Gly Tyr Glu Asn Ser Gly Pro Gly Phe Trp

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Thr Gly Leu Gly Thr Gly Gly Ile Leu Gly Tyr Leu Phe Gly Ser Asn

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Arg Ala Ala Thr Pro Phe Ser Asp Ser Trp Tyr Tyr Pro Ser Tyr Pro

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Pro Ser Tyr Pro Gly Thr Trp Asn Arg Ala Tyr Ser Pro Leu His Gly

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Gly Ser Gly Ser Tyr Ser Val Cys Ser Asn Ser Asp Thr Lys Thr Arg

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Thr Ala Ser Gly Tyr Gly Gly Thr Arg Arg Arg

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<213> Homo sapiens

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Gly Leu His Leu Phe Leu Leu Thr Ala Gly Pro Ala Leu Gly Trp Asn

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Asp Pro Asp Arg Met Leu Leu Arg Asp Val Lys Ala Leu Thr Leu His

35 40 45

Tyr Asp Arg Tyr Thr Thr Ser Arg Arg Leu Asp Pro Ile Pro Gln Leu

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Pro Pro Gly Phe Lys Ser Glu Phe Thr Gly Pro Gln Asn Thr Gly His			
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Gly Ala Thr Ser Gly Phe Gly Ser Ala Phe Thr Gly Gln Gln Gly Tyr			
245	250	255	
Glu Asn Ser Gly Pro Gly Phe Trp Thr Gly Leu Gly Thr Gly Gly Ile			
260	265	270	
Leu Gly Tyr Leu Phe Gly Ser Asn Arg Ala Ala Thr Pro Phe Ser Asp			
275	280	285	
Ser Trp Tyr Tyr Pro Ser Tyr Pro Pro Ser Tyr Pro Gly Thr Trp Asn			
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Arg Ala Tyr Ser Pro Leu His Gly Gly Ser Gly Ser Tyr Ser Val Cys			
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Met

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Ala Ala Ala Cys Gly Pro Gly Ala Ala Gly Tyr Cys Leu Leu Leu Gly

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ttg cat ttg ttt ctg ctg acc gcg ggc cct gcc ctg ggc tgg aac gac 213

Leu His Leu Phe Leu Leu Thr Ala Gly Pro Ala Leu Gly Trp Asn Asp

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cct gac aga atg ttg ctg cgg gat gta aaa gct ctt acc ctc cac tat 261

Pro Asp Arg Met Leu Leu Arg Asp Val Lys Ala Leu Thr Leu His Tyr

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gac cgc tat acc acc tcc cgc agg ctg gat ccc atc cca cag ttg aaa 309

Asp Arg Tyr Thr Thr Ser Arg Arg Leu Asp Pro Ile Pro Gln Leu Lys

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acc atc gtg gta ctc ctt ggg atc gcc ttt gta gtc tat aag ctg ttc 693

Thr Ile Val Val Leu Leu Gly Ile Ala Phe Val Val Tyr Lys Leu Phe

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Leu Ser Asp Gly Gln Tyr Ser Pro Pro Pro Tyr Ser Glu Tyr Pro Pro

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Phe Ser His Arg Tyr Gln Arg Phe Thr Asn Ser Ala Gly Pro Pro Pro

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cca ggc ttt aag tct gag ttc aca gga cca cag aat act ggc cat ggt 837

Pro Gly Phe Lys Ser Glu Phe Thr Gly Pro Gln Asn Thr Gly His Gly

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Ala Thr Ser Gly Phe Gly Ser Ala Phe Thr Gly Gln Gln Gly Tyr Glu

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aat tca gga cca ggg ttc tgg aca ggc ttg gga act ggt gga ata cta 933

Asn Ser Gly Pro Gly Phe Trp Thr Gly Leu Gly Thr Gly Gly Ile Leu

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Gly Tyr Leu Phe Gly Ser Asn Arg Ala Ala Thr Pro Phe Ser Asp Ser

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Trp Tyr Tyr Pro Ser Tyr Pro Pro Ser Tyr Pro Gly Thr Trp Asn Arg
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gct tac tca ccc ctt cat gga ggc tcg ggc agc tat tcg gta tgt tca 1077
 Ala Tyr Ser Pro Leu His Gly Gly Ser Gly Ser Tyr Ser Val Cys Ser
 310 315 320

aac tca gac acg aaa acc aga act gca tca gga tat ggt ggt acc agg 1125
 Asn Ser Asp Thr Lys Thr Arg Thr Ala Ser Gly Tyr Gly Gly Thr Arg
 325 330 335

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 Arg Arg

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- <212> PRT
- <213> Homo sapiens

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Gly Leu Ile Ala Pro Gly Pro Thr Thr Ala Val Ser Tyr Met Ser Val
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Lys Cys Val Asp Ala Arg Lys Asn His His Lys Thr Lys Trp Phe Val
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Pro Trp Gly Pro Asn His Cys Asp Lys Ile Arg Asp Ile Glu Glu Ala
65 70 75 80

Ile Pro Arg Glu Ile Glu Ala Asn Asp Ile Val Phe Ser Val His Ile
85 90 95

Pro Leu Pro His Met Glu Met Ser Pro Trp Phe Gln Phe Met Leu Phe
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cccagaaagg aggcgaggaa ggagggagtg tgtgagagga gggagcaaaa agctcaccct 180

aaaacattta tttcaaggag aaaagaaaaa gggggggcgc aaaa atg gct ggg gca 236

Met Ala Gly Ala

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att ata gaa aac atg agc acc aag aag ctg tgc att gtt ggt ggg att 284

Ile Ile Glu Asn Met Ser Thr Lys Lys Leu Cys Ile Val Gly Gly Ile

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ctg ctc gtg ttc caa atc atc gcc ttt ctg gtg gga ggc ttg att gct 332

Leu Leu Val Phe Gln Ile Ile Ala Phe Leu Val Gly Gly Leu Ile Ala

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cca ggg ccc aca acg gca gtg tcc tac atg tcg gtg aaa tgt gtg gat 380

Pro Gly Pro Thr Thr Ala Val Ser Tyr Met Ser Val Lys Cys Val Asp

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gcc cgt aag aac cat cac aag aca aaa tgg ttc gtg cct tgg gga ccc 428

Ala Arg Lys Asn His His Lys Thr Lys Trp Phe Val Pro Trp Gly Pro

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aat cat tgt gac aag atc cga gac att gaa gag gca att cca agg gaa 476

Asn His Cys Asp Lys Ile Arg Asp Ile Glu Glu Ala Ile Pro Arg Glu

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att gaa gcc aat gac atc gtg ttt tct gtt cac att ccc ctc ccc cac 524

Ile Glu Ala Asn Asp Ile Val Phe Ser Val His Ile Pro Leu Pro His

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atg gag atg agt cct tgg ttc caa ttc atg ctg ttt atc ctg cag ctg 572

Met Glu Met Ser Pro Trp Phe Gln Phe Met Leu Phe Ile Leu Gln Leu

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gac att gcc ttc aag cta aac aac caa atc agt taagtgtact ctcctctcat 625

Asp Ile Ala Phe Lys Leu Asn Asn Gln Ile Ser

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20

25

30

Gly Leu Ile Ala Pro Gly Pro Thr Thr Ala Val Ser Tyr Met Ser Val

35

40

45

Lys Cys Val Asp Ala Arg Lys Asn His His Lys Thr Lys Trp Phe Val

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Pro Ser Gly Met Val Phe His Arg Val

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cccagaaagg aggcgaggaa ggagggagtg tgtgagagga gggagcaaaa agctcacctt 180

aaaacattta tttcaaggag aaaagaaaaa gggggggcgc aaaa atg gct ggg gca 236

Met Ala Gly Ala

att ata gaa aac atg agc acc aag aag ctg tgc att gtt ggt ggg att 284

Ile Ile Glu Asn Met Ser Thr Lys Lys Leu Cys Ile Val Gly Gly Ile

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ctg ctc gtg ttc caa atc atc gcc ttt ctg gtg gga ggc ttg att gct 332

Leu Leu Val Phe Gln Ile Ile Ala Phe Leu Val Gly Gly Leu Ile Ala

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cca ggg ccc aca acg gca gtg tcc tac atg tcg gtg aaa tgt gtg gat 380

Pro Gly Pro Thr Thr Ala Val Ser Tyr Met Ser Val Lys Cys Val Asp

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gcc cgt aag aac cat cac aag aca aaa tgg ttc gtg cct tgg gga ccc 428

Ala Arg Lys Asn His His Lys Thr Lys Trp Phe Val Pro Trp Gly Pro

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aat cat tgt gac aag atc cga gac att gaa gag gca att cca agg gaa 476

Asn His Cys Asp Lys Ile Arg Asp Ile Glu Glu Ala Ile Pro Arg Glu

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Ile Glu Ala Asn Asp Ile Val Phe Ser Val His Ile Pro Leu Pro His

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atg gag atg agt cct tgg ttc caa ttc atg ctg ttt atc ctg cag ctg 572

Met Glu Met Ser Pro Trp Phe Gln Phe Met Leu Phe Ile Leu Gln Leu

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Asp Ile Ala Phe Lys Leu Asn Asn Gln Ile Arg Glu Asn Ala Glu Val

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Ser Met Asp Val Ser Leu Ala Tyr Arg Asp Asp Ala Phe Ala Glu Trp

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Thr Glu Met Ala His Glu Arg Val Pro Arg Lys Leu Lys Cys Thr Phe

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Thr Ser Pro Lys Thr Pro Glu His Glu Gly Arg Tyr Tyr Glu Cys Asp

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Val Leu Pro Tyr Ala Gln His Leu His His Tyr Gly Val Val Leu Glu

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Glu Asp His His Asp Val Pro Thr Pro Ser Ala Ser Gly Lys Ser His

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Leu Cys Pro Trp Asp Phe His Asp Leu Tyr Gln Tyr Pro Ser Gly Met

215

220

225

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Val Phe His Arg Val

230

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22/735

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Ala Ala Lys Asn Phe Glu Asp Val Arg Cys Lys Cys Ile Cys Pro Pro

 35 40 45

Tyr Lys Glu Asn Ser Gly His Ile Tyr Asn Lys Asn Ile Ser Gln Lys

 50 55 60

Asp Cys Asp Cys Leu His Val Val Glu Pro Met Pro Val Arg Gly Pro

65 70 75 80

Asp Val Glu Ala Tyr Cys Leu Arg Cys Glu Cys Lys Tyr Glu Glu Arg

 85 90 95

Ser Ser Val Thr Ile Lys Val Thr Ile Ile Ile Tyr Leu Ser Ile Leu

 100 105 110

Gly Leu Leu Leu Leu Tyr Met Val Tyr Leu Thr Leu Val Glu Pro Ile

 115 120 125

Leu Lys Arg Arg Leu Phe Gly His Ala Gln Leu Ile Gln Ser Asp Asp

 130 135 140

Asp Ile Gly Asp His Gln Pro Phe Ala Asn Ala His Asp Val Leu Ala

145 150 155 160

Arg Ser Arg Ser Arg Ala Asn Val Leu Asn Lys Val Glu Tyr Ala Gln

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Arg His Val Val Leu Ser

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Met Ala Thr Leu Trp Gly Gly Leu Leu

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5

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Arg Leu Gly Ser Leu Leu Ser Leu Ser Cys Leu Ala Leu Ser Val Leu

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Leu Leu Ala Gln Leu Ser Asp Ala Ala Lys Asn Phe Glu Asp Val Arg

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tgt aaa tgt atc tgc cct ccc tat aaa gaa aat tct ggg cat att tat 256

Cys Lys Cys Ile Cys Pro Pro Tyr Lys Glu Asn Ser Gly His Ile Tyr

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aat aag aac ata tct cag aaa gat tgt gat tgc ctt cat gtt gtg gag 304

Asn Lys Asn Ile Ser Gln Lys Asp Cys Asp Cys Leu His Val Val Glu

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65

70

ccc atg cct gtg cgg ggg cct gat gta gaa gca tac tgt cta cgc tgt 352

Pro Met Pro Val Arg Gly Pro Asp Val Glu Ala Tyr Cys Leu Arg Cys

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Glu Cys Lys Tyr Glu Glu Arg Ser Ser Val Thr Ile Lys Val Thr Ile

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Ile Ile Tyr Leu Ser Ile Leu Gly Leu Leu Leu Leu Tyr Met Val Tyr

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ctt act ctg gtt gag ccc ata ctg aag agg cgc ctc ttt gga cat gca 496

Leu Thr Leu Val Glu Pro Ile Leu Lys Arg Arg Leu Phe Gly His Ala

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cag ttg ata cag agt gat gat gat att ggg gat cac cag cct ttt gca 544

Gln Leu Ile Gln Ser Asp Asp Asp Ile Gly Asp His Gln Pro Phe Ala

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Asn Ala His Asp Val Leu Ala Arg Ser Arg Ser Arg Ala Asn Val Leu

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Gln Arg Lys Ser Val Phe Asp Arg His Val Val Leu Ser

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[illegible][illegible][illegible][illegible][illegible]

all other amino acids are present in the protein

35

40

45

Ser Ala Ala Tyr Phe Asp Tyr Lys Asp Glu Ser Gly Phe Pro Lys Pro

50

55

60

Pro Ser Tyr Asn Val Ala Thr Thr Leu Pro Ser Tyr Asp Glu Ala Glu

65

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75

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Arg Thr Lys Ala Glu Ala Thr Ile Pro Leu Val Pro Gly Arg Asp Glu

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95

Asp Phe Val Gly Arg Asp Asp Phe Asp Asp Ala Asp Gln Leu Arg Ile

100

105

110

Gly Asn Asp Gly Ile Phe Met Leu Thr Phe Phe Met Ala Phe Leu Phe

115

120

125

Asn Trp Ile Gly Phe Phe Leu Ser Phe Cys Leu Thr Thr Ser Ala Ala

130

135

140

Gly Arg Tyr Gly Ala Ile Ser Gly Phe Gly Leu Ser Leu Ile Lys Trp

145

150

155

160

Ile Leu Ile Val Arg Phe Ser Thr Tyr Phe Pro Gly Tyr Phe Asp Gly

165

170

175

Gln Tyr Trp Leu Trp Trp Val Phe Leu Val Leu Gly Phe Leu Leu Phe

180

185

190

Leu Arg Gly Phe Ile Asn Tyr Ala Lys Val Arg Lys Met Pro Glu Thr
195 200 205

Phe Ser Asn Leu Pro Arg Thr Arg Val Leu Phe Ile Tyr
210 215 220

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gctcgctctg ctcccttget gccggetgcg cc atg gcg ttg gcg ttg gcg gcg 173
Met Ala Leu Ala Leu Ala Ala
1 5

ctg gcg gcg gtc gag ccg gcc tgc ggc agc cgg tac cag cag ttg cag 221
Leu Ala Ala Val Glu Pro Ala Cys Gly Ser Arg Tyr Gln Gln Leu Gln
10 15 20

aat gaa gaa gag tct gga gaa cct gaa cag gct gca ggt gat gct cct 269

Asn Glu Glu Glu Ser Gly Glu Pro Glu Gln Ala Ala Gly Asp Ala Pro

25 30 35

cca cct tac agc agc att tct gca gag agc gca gca tat ttt gac tac 317

Pro Pro Tyr Ser Ser Ile Ser Ala Glu Ser Ala Ala Tyr Phe Asp Tyr

40 45 50 55

aag gat gag tct ggg ttt cca aag ccc cca tct tac aat gta gct aca 365

Lys Asp Glu Ser Gly Phe Pro Lys Pro Pro Ser Tyr Asn Val Ala Thr

60 65 70

aca ctg ccc agt tat gat gaa gcg gag agg acc aag gct gaa gct act 413

Thr Leu Pro Ser Tyr Asp Glu Ala Glu Arg Thr Lys Ala Glu Ala Thr

75 80 85

atc cct ttg gtt cct ggg aga gat gag gat ttt gtg ggt cgg gat gat 461

Ile Pro Leu Val Pro Gly Arg Asp Glu Asp Phe Val Gly Arg Asp Asp

90 95 100

ttt gat gat gct gac cag ctg agg ata gga aat gat ggg att ttc atg 509

Phe Asp Asp Ala Asp Gln Leu Arg Ile Gly Asn Asp Gly Ile Phe Met

105 110 115

tta act ttt ttc atg gca ttc ctc ttt aac tgg att ggg ttt ttc ctg 557

Leu Thr Phe Phe Met Ala Phe Leu Phe Asn Trp Ile Gly Phe Phe Leu

120 125 130 135

tct ttt tgc ctg acc act tca gct gca gga agg tat ggg gcc att tca 605

Ser Phe Cys Leu Thr Thr Ser Ala Ala Gly Arg Tyr Gly Ala Ile Ser

140

145

150

gga ttt ggt ctc tct cta att aaa tgg atc ctg att gtc agg ttt tcc 653

Gly Phe Gly Leu Ser Leu Ile Lys Trp Ile Leu Ile Val Arg Phe Ser

155

160

165

acc tat ttc cct gga tat ttt gat ggt cag tac tgg ctc tgg tgg gtg 701

Thr Tyr Phe Pro Gly Tyr Phe Asp Gly Gln Tyr Trp Leu Trp Trp Val

170

175

180

ttc ctt gtt tta ggc ttt ctc ctg ttt ctc aga gga ttt atc aat tat 749

Phe Leu Val Leu Gly Phe Leu Leu Phe Leu Arg Gly Phe Ile Asn Tyr

185

190

195

gca aaa gtt cgg aag atg cca gaa act ttc tca aat ctc ccc agg acc 797

Ala Lys Val Arg Lys Met Pro Glu Thr Phe Ser Asn Leu Pro Arg Thr

200

205

210

215

aga gtt ctc ttt att tat taaagatggt ttctggcaaa ggccttctg 845

Arg Val Leu Phe Ile Tyr

220

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gaacacagag gaataatcac ctgctttaaa aaaataaagt actgttgaaa agatcatttc 965

tctctatttg ttcttagtg taaaatttta atagttaatg cagaattctg taatcattga 1025

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gccttatata ttgtttgtag tcattttaag tagcatgagc catgtccctg tagtcggtag 1145

ggggcagtct tgctttattc atcctccatc tcaaaatgaa cttggaatta aatattgtaa 1205

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<212> PRT

<213> Homo sapiens

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Glu Glu Asp Asn Ser Glu Ser Ser Ala Ile Glu Gln Pro Pro Thr Ser

20 25 30

Asn Pro Ala Pro Gln Ile Val Gln Ala Ala Ser Ser Ala Pro Ala Leu

35 40 45

Glu Thr Asp Ser Ser Pro Pro Pro Tyr Ser Ser Ile Thr Val Glu Val

50 55 60

Pro Thr Thr Ser Asp Thr Glu Val Tyr Gly Glu Phe Tyr Pro Val Pro

65 70 75 80

Pro Pro Tyr Ser Val Ala Thr Ser Leu Pro Thr Tyr Asp Glu Ala Glu

85 90 95

Lys Ala Lys Ala Ala Ala Met Ala Ala Ala Ala Glu Thr Ser Gln

100 105 110

Arg Ile Gln Glu Glu Glu Cys Pro Pro Arg Asp Asp Phe Ser Asp Ala

115 120 125

Asp Gln Leu Arg Val Gly Asn Asp Gly Ile Phe Met Leu Ala Phe Phe
130 135 140

Met Ala Phe Ile Phe Asn Trp Leu Gly Phe Cys Leu Ser Phe Cys Ile
145 150 155 160

Thr Asn Thr Ile Ala Gly Arg Tyr Gly Ala Ile Cys Gly Phe Gly Leu
165 170 175

Ser Leu Ile Lys Trp Ile Leu Ile Val Arg Phe Ser Asp Tyr Phe Thr
180 185 190

Gly Tyr Phe Asn Gly Gln Tyr Trp Leu Trp Trp Ile Phe Leu Val Leu
195 200 205

Gly Leu Leu Leu Phe Phe Arg Gly Phe Val Asn Tyr Leu Lys Val Arg
210 215 220

Asn Met Ser Glu Ser Met Ala Ala Ala His Arg Thr Arg Tyr Phe Phe
225 230 235 240

Leu Leu

<210> 14

<211> 2324

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (13).. (738)

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Leu Leu Asn Glu Glu Asp Asn Ser Glu Ser Ser Ala Ile Glu Gln Pro

15 20 25

cct act tca aac cca gca ccg cag att gtg cag gct gcg tct tca gca 147

Pro Thr Ser Asn Pro Ala Pro Gln Ile Val Gln Ala Ala Ser Ser Ala

30 35 40 45

cca gca ctt gaa act gac tct tcc cct cca cca tat agt agt att act 195

Pro Ala Leu Glu Thr Asp Ser Ser Pro Pro Pro Tyr Ser Ser Ile Thr

50 55 60

gtg gaa gta cct aca act tca gat aca gaa gtt tac ggt gag ttt tat 243

Val Glu Val Pro Thr Thr Ser Asp Thr Glu Val Tyr Gly Glu Phe Tyr

65 70 75

ccc gtg cca cct ccc tat agc gtt gct acc tct ctt cct aca tac gat 291

Pro Val Pro Pro Pro Tyr Ser Val Ala Thr Ser Leu Pro Thr Tyr Asp

80

85

90

gaa gct gag aag gct aaa gct gct gca atg gca gct gca gca gca gaa 339
 Glu Ala Glu Lys Ala Lys Ala Ala Ala Met Ala Ala Ala Ala Glu
 95 100 105

aca tct caa aga att cag gag gaa gag tgt cca cca aga gat gac ttc 387
 Thr Ser Gln Arg Ile Gln Glu Glu Glu Cys Pro Pro Arg Asp Asp Phe
 110 115 120 125

agt gat gca gac cag ctc aga gtg ggg aat gat ggc att ttc atg ctg 435
 Ser Asp Ala Asp Gln Leu Arg Val Gly Asn Asp Gly Ile Phe Met Leu
 130 135 140

gca ttt ttc atg gca ttt att ttc aac tgg ctt gga ttt tgt tta tcc 483
 Ala Phe Phe Met Ala Phe Ile Phe Asn Trp Leu Gly Phe Cys Leu Ser
 145 150 155

ttc tgt atc acc aat acc ata gct gga agg tat ggt gct atc tgc gga 531
 Phe Cys Ile Thr Asn Thr Ile Ala Gly Arg Tyr Gly Ala Ile Cys Gly
 160 165 170

ttt ggc ctt tcc ttg atc aaa tgg atc ctt att gtc agg ttt tct gat 579
 Phe Gly Leu Ser Leu Ile Lys Trp Ile Leu Ile Val Arg Phe Ser Asp
 175 180 185

tat ttt act gga tat ttc aat gga cag tat tgg ctt tgg tgg ata ttt 627
 Tyr Phe Thr Gly Tyr Phe Asn Gly Gln Tyr Trp Leu Trp Trp Ile Phe
 190 195 200 205

ctt gta ctt ggc ctg ctc ctt ttc ttc aga gga ttt gtt aat tat cta 675

Leu Val Leu Gly Leu Leu Leu Phe Phe Arg Gly Phe Val Asn Tyr Leu

210

215

220

aaa gtc aga aac atg tct gaa agt atg gca gct gct cat aga aca agg 723

Lys Val Arg Asn Met Ser Glu Ser Met Ala Ala Ala His Arg Thr Arg

225

230

235

tat ttc ttc tta ttg tagagactgc atcaaccgga cattcctttc ttataccaat 778

Tyr Phe Phe Leu Leu

240

gtgaaatttc cagatcatct gtaaacctac aactttaata gaagactact aataacagaa 838

gacaaattag tgaagaaaag acggagtttc gaaattgaat ggcaggggtgg tttttgctta 898

caagccattt ctgttcattc tttaagtatc tatatttcat ttgttttgca catatgcata 958

tgtgcccatt taagatattt gcatatactt gatagaaacc ataaagttgt agcagttaag 1018

tccagtcaca tttggttaat cagtgtttga tataattgaa agagttgagt ggataaacag 1078

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atttgtcaga tttttgaaca tgatatttac attattattt aggaaaactc ttcctgtaaa 1318

taaccatgca taacttactt tctgcaatgt tttcttagaa attgtgtcca gatagctttc 1378

actaatttta aattaagtga actaaatata tatgtgtata tgtatacaca tatatataca 1438

cacacacata tatatattta gaaacgtgag tgttaaagat agaatttggt ttaggacaaa 1498

ttttaagaaa atgtgggaat accaaatgtc ctttataaga aaaataaatt ttattttaag 1558

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aagagatctt gcaggaagag attgtattag atattatatt tatttcattt aagataattt 1678

tcaaagttaa ttttctaaat aagataattc tcatttgtgt ttgtctttta aaaggccaat 1738

aaaatatctt tcagtatcat tgtaataatt ttttagagtt taatttgtaa agcttagcaa 1798

ataaaatctt gtactatgaa tagcttcttg ctttatgact ttaggattaa cttgtaaaaa 1858

acatatcctg aactgagata tgcaaaatac tcattttcaa gttatggaaa tgtgtttgtg 1918

gcatatagga ctgtggggtc tgtgtgtgta gtgagagtgt gtagccacta ttataactgg 1978

aatttaattt acattcataa actactatat ttcccatctt gcaaatcatt ttatgtctca 2038

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<212> PRT

<213> Homo sapiens

<400> 15

Met Asp His His Gln Pro Gly Thr Gly Arg Tyr Gln Val Leu Leu Asn

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Glu Glu Asp Asn Ser Glu Ser Ser Ala Ile Glu Gln Pro Pro Thr Ser

20 25 30

Asn Pro Ala Pro Gln Ile Val Gln Ala Val Ser Ser Ala Pro Ala Leu

35 40 45

Glu Thr Asp Ser Ser Pro Pro Pro Tyr Ser Ser Ile Thr Val Glu Val

50 55 60

Pro Thr Thr Ser Asp Thr Glu Val Tyr Gly Glu Phe Tyr Pro Val Pro

65 70 75 80

Pro Pro Tyr Ser Val Ala Thr Ser Leu Pro Thr Tyr Asp Glu Ala Glu
85 90 95

Lys Ala Lys Ala Ala Ala Met Ala Ala Ala Ala Ala Glu Thr Ser Gln
100 105 110

Arg Ile Gln Glu Glu Glu Cys Pro Pro Arg Asp Asp Phe Ser Asp Ala
115 120 125

Asp Gln Leu Arg Val Gly Asn Asp Gly Ile Phe Met Leu Ala Phe Phe
130 135 140

Met Ala Phe Ile Phe Asn Trp Leu Gly Phe Cys Leu Ser Phe Cys Ile
145 150 155 160

Thr Asn Thr Ile Ala Gly Arg Tyr Gly Ala Ile Cys Gly Phe Gly Leu
165 170 175

Ser Leu Ile Lys Trp Ile Leu Ile Val Arg Phe Ser Asp Tyr Phe Thr
180 185 190

Gly Tyr Phe Asn Gly Gln Tyr Trp Leu Trp Trp Ile Phe Leu Val Leu
195 200 205

Gly Leu Leu Leu Phe Phe Arg Gly Phe Val Asn Tyr Leu Lys Val Arg
210 215 220

Asn Met Ser Glu Ser Met Ala Ala Ala His Arg Thr Arg Tyr Phe Phe
225 230 235 240

$\frac{d}{dt} \left(\frac{1}{\rho} \right) = - \frac{1}{\rho^2} \frac{d\rho}{dt}$

⟨213⟩ Homo sapiens

<222> (13).. (738)

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25

45

41/735

50

55

60

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Val Glu Val Pro Thr Thr Ser Asp Thr Glu Val Tyr Gly Glu Phe Tyr
65 70 75

ccc gtg cca cct ccc tat agc gtt gct acc tct ctt cct aca tac gat 291
Pro Val Pro Pro Pro Tyr Ser Val Ala Thr Ser Leu Pro Thr Tyr Asp
80 85 90

gaa gct gag aag gct aaa gct gct gca atg gca gct gca gca gca gaa 339
Glu Ala Glu Lys Ala Lys Ala Ala Ala Met Ala Ala Ala Ala Ala Glu
95 100 105

aca tct caa aga att cag gag gaa gag tgt cca cca aga gat gac ttc 387
Thr Ser Gln Arg Ile Gln Glu Glu Glu Cys Pro Pro Arg Asp Asp Phe
110 115 120 125

agt gat gca gac cag ctc aga gtg ggg aat gat ggc att ttc atg ctg 435
Ser Asp Ala Asp Gln Leu Arg Val Gly Asn Asp Gly Ile Phe Met Leu
130 135 140

gca ttt ttc atg gca ttt att ttc aac tgg ctt gga ttt tgt tta tcc 483
Ala Phe Phe Met Ala Phe Ile Phe Asn Trp Leu Gly Phe Cys Leu Ser
145 150 155

ttc tgt atc acc aat acc ata gct gga agg tat ggt gct atc tgc gga 531
Phe Cys Ile Thr Asn Thr Ile Ala Gly Arg Tyr Gly Ala Ile Cys Gly
160 165 170

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cacacacata tatatattta gaaacgtgag tgttaaagat agaatttggt ttaggacaaa 1498

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aagagatctt gcaggaagag attgtattag atatttatatt tatttcattt aagataattt 1678

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35

40

45

Leu Pro Pro Gly Asp Arg Gly Cys Arg Asn Gly Gly Gly Arg Gly Pro
50 55 60

Ala Ala Thr Thr Ser Ser Thr Gly Val Ala Val Gly Ala Glu His Gly
65 70 75 80

Glu Asp Ser Leu Ser Arg Lys Pro Asp Pro Glu Pro Gly Arg Met Asp
85 90 95

His His Gln Pro Gly Thr Gly Arg Tyr Gln Val Leu Leu Asn Glu Glu
100 105 110

Asp Asn Ser Glu Ser Ser Ala Ile Glu Gln Pro Pro Thr Ser Asn Pro
115 120 125

Ala Pro Gln Ile Val Gln Ala Val Ser Ser Ala Pro Ala Leu Glu Thr
130 135 140

Asp Ser Ser Pro Pro Pro Tyr Ser Ser Ile Thr Val Glu Val Pro Thr
145 150 155 160

Thr Ser Asp Thr Glu Val Tyr Gly Glu Phe Tyr Pro Val Pro Pro Pro
165 170 175

Tyr Ser Val Ala Thr Ser Leu Pro Thr Tyr Asp Glu Ala Glu Lys Ala
180 185 190

Lys Ala Ala Ala Met Ala Ala Ala Ala Glu Thr Ser Gln Arg Ile

195

200

205

Gln Glu Glu Glu Cys Pro Pro Arg Asp Asp Phe Ser Asp Ala Asp Gln

210

215

220

Leu Arg Val Gly Asn Asp Gly Ile Phe Met Leu Ala Phe Phe Met Ala

225

230

235

240

Phe Ile Phe Asn Trp Leu Gly Phe Cys Leu Ser Phe Cys Ile Thr Asn

245

250

255

Thr Ile Ala Gly Arg Tyr Gly Ala Ile Cys Gly Phe Gly Leu Ser Leu

260

265

270

Ile Lys Trp Ile Leu Ile Val Arg Phe Ser Asp Tyr Phe Thr Gly Tyr

275

280

285

Phe Asn Gly Gln Tyr Trp Leu Trp Trp Ile Phe Leu Val Leu Gly Leu

290

295

300

Leu Leu Phe Phe Arg Gly Phe Val Asn Tyr Leu Lys Val Arg Asn Met

305

310

315

320

Ser Glu Ser Met Ala Ala Ala His Arg Thr Arg Tyr Phe Phe Leu Leu

325

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335

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<212> DNA

<213> Homo sapiens

<220>

<221> CDS

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Met Ala

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Arg Arg Arg Ser Gln Arg Val Cys Ala Ser Gly Pro Ser Met Leu Asn

5

10

15

agc gcg cgc ggc gcc ccg gag ctt ctc cgc gga acc gcg acc aac gcg 154

Ser Ala Arg Gly Ala Pro Glu Leu Leu Arg Gly Thr Ala Thr Asn Ala

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25

30

gag gtc tcg gcg gcc gct gcg gga gcc aca gga agt gaa gag ctt ccg 202

Glu Val Ser Ala Ala Ala Ala Gly Ala Thr Gly Ser Glu Glu Leu Pro

35

40

45

50

ccg gga gac cgc ggc tgc agg aac gga ggc gga agg ggc cct gcg gcg 250

Pro Gly Asp Arg Gly Cys Arg Asn Gly Gly Gly Arg Gly Pro Ala Ala

55

60

65

acg acg tcg tcg acg ggg gtg gcc gtg gga gct gag cac gga gaa gac 298

Thr Thr Ser Ser Thr Gly Val Ala Val Gly Ala Glu His Gly Glu Asp

70

75

80

tcc ctc tct cgg aag ccg gat ccc gag ccg ggc agg atg gat cac cac 346

Ser Leu Ser Arg Lys Pro Asp Pro Glu Pro Gly Arg Met Asp His His

85

90

95

cag ccg ggg act ggg cgc tac cag gtg ctt ctt aat gaa gag gat aac 394

Gln Pro Gly Thr Gly Arg Tyr Gln Val Leu Leu Asn Glu Glu Asp Asn

100

105

110

tca gaa tca tcg gct ata gag cag cca cct act tca aac cca gca ccg 442

Ser Glu Ser Ser Ala Ile Glu Gln Pro Pro Thr Ser Asn Pro Ala Pro

115

120

125

130

cag att gtg cag gct gtg tct tca gca cca gca ctt gaa act gac tct 490

Gln Ile Val Gln Ala Val Ser Ser Ala Pro Ala Leu Glu Thr Asp Ser

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Ser Pro Pro Pro Tyr Ser Ser Ile Thr Val Glu Val Pro Thr Thr Ser

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Asp Thr Glu Val Tyr Gly Glu Phe Tyr Pro Val Pro Pro Pro Tyr Ser

165

170

175

gtt gct acc tct ctt cct aca tac gat gaa gct gag aag gct aaa gct 634

Val Ala Thr Ser Leu Pro Thr Tyr Asp Glu Ala Glu Lys Ala Lys Ala

180

185

190

gct gca atg gca gct gca gca gca gaa aca tct caa aga att cag gag 682

Ala Ala Met Ala Ala Ala Ala Ala Glu Thr Ser Gln Arg Ile Gln Glu

195

200

205

210

gaa gag tgt cca cca aga gat gac ttc agt gat gca gac cag ctc aga 730

Glu Glu Cys Pro Pro Arg Asp Asp Phe Ser Asp Ala Asp Gln Leu Arg

215

220

225

gtg ggg aat gat ggc att ttc atg ctg gca ttt ttc atg gca ttt att 778

Val Gly Asn Asp Gly Ile Phe Met Leu Ala Phe Phe Met Ala Phe Ile

230

235

240

ttc aac tgg ctt gga ttt tgt tta tcc ttc tgt atc acc aat acc ata 826

Phe Asn Trp Leu Gly Phe Cys Leu Ser Phe Cys Ile Thr Asn Thr Ile

245

250

255

gct gga agg tat ggt gct atc tgc gga ttt ggc ctt tcc ttg atc aaa 874

Ala Gly Arg Tyr Gly Ala Ile Cys Gly Phe Gly Leu Ser Leu Ile Lys

260

265

270

tgg atc ctt att gtc agg ttt tct gat tat ttt act gga tat ttc aat 922

Trp Ile Leu Ile Val Arg Phe Ser Asp Tyr Phe Thr Gly Tyr Phe Asn

275

280

285

290

gga cag tat tgg ctt tgg tgg ata ttt ctt gta ctt ggc ctg ctc ctt 970

Gly Gln Tyr Trp Leu Trp Trp Ile Phe Leu Val Leu Gly Leu Leu Leu

295

300

305

ttc ttc aga gga ttt gtt aat tat cta aaa gtc aga aac atg tct gaa 1018
Phe Phe Arg Gly Phe Val Asn Tyr Leu Lys Val Arg Asn Met Ser Glu

310

315

320

agt atg gca gct gct cat aga aca agg tat ttc ttc tta ttg 1060
Ser Met Ala Ala Ala His Arg Thr Arg Tyr Phe Phe Leu Leu

325

330

335

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gtaaacttac aactttaata gaagactact aataacagaa gacaaattag tgaagaaaag 1180

acggagtttc gaaattgaat ggcagggtgg tttttgctta caagccattt ctgttcattc 1240

tttaagtatc tatatttcat ttgttttgca catatgcata tgtgcccatt taagatatatt 1300

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tgatatattac attattattt aggaaaactc ttcctgtaaa taacctatgca taacttactt 1660

actactaaaa ggtacatcta actattcagg gacatttttc catttcctaaa aaataaaatt 2560

tattatgctt tataacctct tctgtatttt ctaatttttt cattgtcttt gataaataaa 2620

acagttttgt tttgct 2636

<210> 19

<211> 336

<212> PRT

<213> Homo sapiens

<400> 19

Met Ala Arg Arg Arg Ser Gln Arg Val Cys Ala Ser Gly Pro Ser Met

1 5 10 15

Leu Asn Ser Ala Arg Gly Ala Pro Glu Leu Leu Arg Gly Thr Ala Thr

20 25 30

Asn Ala Glu Val Ser Ala Ala Ala Ala Gly Ala Thr Gly Ser Glu Glu

35 40 45

Leu Pro Pro Gly Asp Arg Gly Cys Arg Asn Gly Gly Gly Arg Gly Pro

50 55 60

Ala Ala Thr Thr Ser Ser Thr Gly Val Ala Val Gly Ala Glu His Gly

65 70 75 80

Glu Asp Ser Leu Ser Arg Lys Pro Asp Pro Glu Pro Gly Arg Met Asp

and the following conditions are satisfied:

250

260

270

275

285

290

300

305

315

320

325

335

<211> 2636

〈213〉 Homo sapiens

<221> CDS

<400> 20

cttacttttc catctctctcc caccagcta taccctccca ctggcggcgc gg atg gca 58

Met Ala

1

cgc cgg cgg agc cag cga gtc tgc gcg agc ggt ccg agc atg ctc aat 106

Arg Arg Arg Ser Gln Arg Val Cys Ala Ser Gly Pro Ser Met Leu Asn

5

10

15

agc gcg cgc ggc gcc ccg gag ctt ctc cgc gga acc gcg acc aac gcg 154

Ser Ala Arg Gly Ala Pro Glu Leu Leu Arg Gly Thr Ala Thr Asn Ala

20

25

30

gag gtc tcg gcg gcc gct gcg gga gcc aca gga agt gaa gag ctt ccg 202

Glu Val Ser Ala Ala Ala Ala Gly Ala Thr Gly Ser Glu Glu Leu Pro

35

40

45

50

ccg gga gac cgc ggc tgc agg aac gga ggc gga agg ggc cct gcg gcg 250

Pro Gly Asp Arg Gly Cys Arg Asn Gly Gly Gly Arg Gly Pro Ala Ala

55

60

65

acg acg tcg tcg acg ggg gtg gcc gtg gga gct gag cac gga gaa gac 298

Thr Thr Ser Ser Thr Gly Val Ala Val Gly Ala Glu His Gly Glu Asp

70

75

80

tcc ctc tct cgg aag ccg gat ccc gag ccg ggc agg atg gat cac cac 346

Ser Leu Ser Arg Lys Pro Asp Pro Glu Pro Gly Arg Met Asp His His

85

90

95

cag ccg ggg act ggg cgc tac cag gtg ctt ctt aat gaa gag gat aac 394

Gln Pro Gly Thr Gly Arg Tyr Gln Val Leu Leu Asn Glu Glu Asp Asn

100 105 110

tca gaa tca tgc gct ata gag cag cca cct act tca aac cca gca ccg 442

Ser Glu Ser Ser Ala Ile Glu Gln Pro Pro Thr Ser Asn Pro Ala Pro

115 120 125 130

cag att gtg cag gct gcg tct tca gca cca gca ctt gaa act gac tct 490

Gln Ile Val Gln Ala Ala Ser Ser Ala Pro Ala Leu Glu Thr Asp Ser

135 140 145

tcc cct cca cca tat agt agt att act gtg gaa gta cct aca act tca 538

Ser Pro Pro Pro Tyr Ser Ser Ile Thr Val Glu Val Pro Thr Thr Ser

150 155 160

gat aca gaa gtt tac ggt gag ttt tat ccc gtg cca cct ccc tat agc 586

Asp Thr Glu Val Tyr Gly Glu Phe Tyr Pro Val Pro Pro Pro Tyr Ser

165 170 175

gtt gct acc tct ctt cct aca tac gat gaa gct gag aag gct aaa gct 634

Val Ala Thr Ser Leu Pro Thr Tyr Asp Glu Ala Glu Lys Ala Lys Ala

180 185 190

gct gca atg gca gct gca gca gca gaa aca tct caa aga att cag gag 682

Ala Ala Met Ala Ala Ala Ala Glu Thr Ser Gln Arg Ile Gln Glu

195 200 205 210

gaa gag tgt cca cca aga gat gac ttc agt gat gca gac cag ctc aga 730

Glu Glu Cys Pro Pro Arg Asp Asp Phe Ser Asp Ala Asp Gln Leu Arg

215

220

225

gtg ggg aat gat ggc att ttc atg ctg gca ttt ttc atg gca ttt att 778

Val Gly Asn Asp Gly Ile Phe Met Leu Ala Phe Phe Met Ala Phe Ile

230

235

240

ttc aac tgg ctt gga ttt tgt tta tcc ttc tgt atc acc aat acc ata 826

Phe Asn Trp Leu Gly Phe Cys Leu Ser Phe Cys Ile Thr Asn Thr Ile

245

250

255

gct gga agg tat ggt gct atc tgc gga ttt ggc ctt tcc ttg atc aaa 874

Ala Gly Arg Tyr Gly Ala Ile Cys Gly Phe Gly Leu Ser Leu Ile Lys

260

265

270

tgg atc ctt att gtc agg ttt tct gat tat ttt act gga tat ttc aat 922

Trp Ile Leu Ile Val Arg Phe Ser Asp Tyr Phe Thr Gly Tyr Phe Asn

275

280

285

290

gga cag tat tgg ctt tgg tgg ata ttt ctt gta ctt ggc ctg ctc ctt 970

Gly Gln Tyr Trp Leu Trp Trp Ile Phe Leu Val Leu Gly Leu Leu Leu

295

300

305

ttc ttc aga gga ttt gtt aat tat cta aaa gtc aga aac atg tct gaa 1018

Phe Phe Arg Gly Phe Val Asn Tyr Leu Lys Val Arg Asn Met Ser Glu

310

315

320

agt atg gca gct gct cat aga aca agg tat ttc ttc tta ttg 1060

Ser Met Ala Ala Ala His Arg Thr Arg Tyr Phe Phe Leu Leu

325

330

335

tagagactgc atcaaccgga cattcctttc ttataccaat gtgaaatttc cagatcatct 1120

gtaaacctac aactttaata gaagactact aataacagaa gacaaattag tgaagaaaag 1180

acggagtttc gaaattgaat ggcagggtgg tttttgctta caagccattt ctgttcattc 1240

tttaagtatc tatatttcat ttgttttgca catatgcata tgtgceccatt taagatatit 1300

gcatatactt gatagaaacc ataaagttgt agcagttaag tccagtcaca tttggttaat 1360

cagtgtttga tataattgaa agagttgagt ggataaacag tcttccagct tgtaaattgcc 1420

attgacttct gacctgacat ttagtataat aaaaatgaaa ttcttaacca tgtcaaattga 1480

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tgatatttac attattattt aggaaaactc ttctgtataa taacctatgca taacttactt 1660

tctgcaatgt tttcttagaa attgtgtcca gatagctttc actaatttta aattaagtga 1720

actaaatata tatgtgtata tgtatacaca tatatataca cacacacata tatatatit 1780

gaaacgtgag tgtaaagat agaatttggt ttaggacaaa ttttaagaaa atgtgggaat 1840

accaaattgc ctttataaga aaaataaatt ttgttttaag ggacatacca gttttaggga 1900

ttttcagatg ggaagctgca ttttttaggat tgcccatctt aagagatctt gcaggaagag 1960

attgtattag atattatatt tatttcattt aagataattt tcaaagttaa ttttctaaat 2020

aagataattc tcatttgtgt ttgtctttta aaaggccaat aaaatatctt tcagtatcat 2080

tgtaataatt ttttagagtt taatttgtaa agcttagcaa ataaaatctt gtactatgaa 2140

tagcttcttg ctttatgact ttaggattaa cttgtaaaaa acatatcctg aactgagata 2200

tgcaaaatac tcattttcaa gttatggaaa tgtgtttgtg gcatatagga ctgtggggtc 2260

tgtgtgtgta gtgagagtgt gtagccacta ttataactgg aatttaattt acattcataa 2320

actactatat ttcccatctt gcaaatcatt ttatgtctca tctgtttttc ctttcggtta 2380

tatcttttgt tttgaatacc aacatttaaa atgatgggtat tttatctttt aaacttaaaa 2440

attatttaat acagctatat ggaccttata aaattgattt cttatttatt attagacatt 2500

actactaaaa ggtacatcta actattcagg gacatttttc catttccaaa aaataaaaatt 2560

tattatgctt tataacctct tctgtatttt ctaatttttt cattgtcttt gataaataaa 2620

acagttttgt tttgct 2636

<210> 21

<211> 76

<212> PRT

<213> Homo sapiens

<400> 21

Met Val Cys Ile Pro Cys Ile Val Ile Pro Val Leu Leu Trp Ile Tyr

1

5

10

15

Lys Lys Phe Leu Glu Pro Tyr Ile Tyr Pro Leu Val Ser Pro Phe Val

20

25

30

Ser Arg Ile Trp Pro Lys Lys Ala Ile Gln Glu Ser Asn Asp Thr Asn

35

40

45

Lys Gly Lys Val Asn Phe Lys Gly Ala Asp Met Asn Gly Leu Pro Thr

50

55

60

Lys Gly Pro Thr Glu Ile Cys Asp Lys Lys Lys Asp

65

70

75

<210> 22

<211> 1085

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (176).. (403)

[illegible]

gcagagtcct aggcggtgcg cggcctcctg cctcctccct cctcggcggt cgcgggccgc 120

Met

1

Val Cys Ile Pro Cys Ile Val Ile Pro Val Leu Leu Trp Ile Tyr Lys

5

10

15

Lys Phe Leu Glu Pro Tyr Ile Tyr Pro Leu Val Ser Pro Phe Val Ser

20

25

30

Arg Ile Trp Pro Lys Lys Ala Ile Gln Glu Ser Asn Asp Thr Asn Lys

35

40

45

Gly Lys Val Asn Phe Lys Gly Ala Asp Met Asn Gly Leu Pro Thr Lys

50

55

60

65

Gly Pro Thr Glu Ile Cys Asp Lys Lys Lys Asp

70

75

accccatcat ttaaaaaatg gacctgataa tatgaagcat cttccttgta attgtctctg 483

acctttttat ctgagaccgg aattcaggat aggagtctag atatttacct gatactaate 543

aggaaatata tgatatccgt atttaaaatg tagttagtta tatttaatga cctcattcct 603

aagttccttt ttcgttaatg tagctttcat ttctgttatt gctgtttgaa taatatgatt 663

aatagaagg ttgtgccag tagacattat gttactaaat cagcacttta aaatctttgg 723

ttctctaatt catatgaatt tgctgtttgc tctaatttct ttgggctctt ctaatttgag 783

tggagtacaa ttttgttgtg aaacagtcca gtgaaactgt gcagggaat gaaggtagaa 843

ttttgggagg taataatgat gtgaaacata aagatttaat aattactgtc caacacagtg 903

gagcagcttg tccacaaata tagtaattac tattttattgc tctaaggaag attaaaaaaa 963

gatagggaac agggggaaac ttctttgaaa aatgaaacat ctgttacatt aatgtctaatt 1023

tataaaattt taatccttac tgcatttctt ctgttcttac aaatgtatta aacattcagt 1083

tt 1085

<210> 23

<211> 84

<212> PRT

<213> Homo sapiens

<400> 23

Met Ala Ile Lys Phe Leu Glu Val Ile Lys Pro Phe Cys Val Ile Leu

1 5 10 15

Pro Glu Ile Gln Lys Pro Glu Arg Lys Ile Gln Phe Lys Glu Lys Val

20 25 30

Leu Trp Thr Ala Ile Thr Leu Phe Ile Phe Leu Val Cys Cys Gln Ile

35 40 45

Pro Leu Phe Gly Ile Met Ser Ser Asp Ser Ala Asp Pro Phe Tyr Trp

50 55 60

Met Arg Val Ile Leu Ala Ser Asn Arg Gly Thr Leu Met Glu His Ser

65 70 75 80

Leu Ser Gly Leu

<210> 24

<211> 1593

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (65).. (316)

<400> 24

agcgtgcct cacgcggagc agagctgagc tgaagcggga cccggagccc gagcagccgc 60

cgcc atg gca atc aaa ttt ctg gaa gtc atc aag ccc ttc tgt gtc atc 109

Met Ala Ile Lys Phe Leu Glu Val Ile Lys Pro Phe Cys Val Ile

1 5 10 15

ctg ccg gaa att cag aag cca gag agg aag att cag ttt aag gag aaa 157

Leu Pro Glu Ile Gln Lys Pro Glu Arg Lys Ile Gln Phe Lys Glu Lys

20 25 30

gtg ctg tgg acc gct atc acc ctc ttt atc ttc tta gtg tgc tgc cag 205

Val Leu Trp Thr Ala Ile Thr Leu Phe Ile Phe Leu Val Cys Cys Gln

35 40 45

att ccc ctg ttt ggg atc atg tct tca gat tca gct gac cct ttc tat 253

Ile Pro Leu Phe Gly Ile Met Ser Ser Asp Ser Ala Asp Pro Phe Tyr

50 55 60

tgg atg aga gtg att cta gcc tct aac aga ggc aca ttg atg gag cac 301

Trp Met Arg Val Ile Leu Ala Ser Asn Arg Gly Thr Leu Met Glu His

65 70 75

tct ctc tct ggc ctt tagggagtcc cctcttagga caggcactgc ccagcagcaa 356

Ser Leu Ser Gly Leu

80

gggcagcaga gttgggtgct aagatcctga ggagctcgag gtttcgagct ggctttagac 416

attggtggga ccaaggatgt ttgacagat gccctgatcc taagaagggg gcctgggggt 476

gcgtgcagcc tgcggggag acccaactct gtgcacctat tggctcttct agctgactct 536

tctcggtggg cttagagtct gcctgtttct gctagctccg tgtttagtcc acttgggtca 596

tcagctctgc caagctgagc ctggccaagc taggtggaca gacccttgca gtgatgtccg 656

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caccttctgg gctgaagatc acccagctgt gttcagaatt ttcttactgt gcttaggact 836

gcacgcaagt gagcagacac caccgacttc ctttctgcgt caccagtgtc gtcagcagag 896

agaggacagc acaggctcaa gtttggtagt gaagtcaggt tcgggggtgca tgggctgtgg 956

tggtggtgat cagttgctcc agtggttgaa ataagaagac tcatgtttat gtctggaata 1016

agttctgttt gtgctgacag gtgacctgac tggcagtgtc agccaggaaa cagagtgacc 1076

aagggacaag aagggacttg cctaaagcca cccagcaact cagcagcaga accaagatgg 1136

gccccaggt cctccatag gccagggt taccacccta tcacagtggt ccttgtctag 1196

accagtcct gagcagggga gaggtcttg agacctgat cctctctacc cacatggttc 1256

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (114).. (650)

<400> 26

gtgtctctcg gcggagctgc tgtgcagtgg aacgcgctgg gccgcgggca gcgtcacctc 60

acgcggagca gagctgagct gaagcgggac ccggagcccg agcagccgcc gcc atg 116

Met

1

gca atc aaa ttt ctg gaa gtc atc aag ccc ttc tgt gtc atc ctg ccg 164

Ala Ile Lys Phe Leu Glu Val Ile Lys Pro Phe Cys Val Ile Leu Pro

5

10

15

gaa att cag aag cca gag agg aag att cag ttt aag gag aaa gtg ctg 212

Glu Ile Gln Lys Pro Glu Arg Lys Ile Gln Phe Lys Glu Lys Val Leu

20

25

30

tgg acc gct atc acc ctc ttt atc ttc tta gtg tgc tgc cag att ccc 260

Trp Thr Ala Ile Thr Leu Phe Ile Phe Leu Val Cys Cys Gln Ile Pro

35

40

45

ctg ttt ggg atc atg tct tca gat tca gct gac ccg gtc cat gca gtt 308

Leu Phe Gly Ile Met Ser Ser Asp Ser Ala Asp Pro Val His Ala Val

50

55

60

65

70/735

[illegible]

aaggggagct ctcacatgg cgcgtgctgc tgcggcatat ggacttttaa taatgttttt 760

tgcttttttat cctggcactg gcaaaaagaa ctgtgaaagt gaattttattc agccgactgc 880

tttgacatt ctcagtgtg tatgctgtg cagccgtctc acctgtttcc ccacaaaggg 1000

gggtgtgaag ctgggagcag atcatgtatt tcccggagac atgggacctt gctggcatgt 1120

tgttttccct tattttaaaa gtgatttttt taaggacaga acttcttcca aaagagaggg 1240

atggctttcc cagaagacac tctggagacc ttgctggcag tgctagccag gaaacagagt 1300

gaccaagggga caagaagggga cttgcctaaa gccacccagc aactcagcag cagaaccaag 1360

atgggcecca ggctcctcca tatggcccag ggcttaccac cctatcacac gtggcettgt 1420

ctagaccag tctgagcag gggagaggct cttgagacct gatgccctcc taccacatg 1480

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gctgggcctt gcaaggccca cactcaagcc ctgtgggtga tggtcacggt ggggtgggtgg 1720

gggctgaccc cagcttcag gggactgtca ctgtggacgc caaaatggca taactsasat 1780

aaggtgaata agtgacaaat aaagccagtt ttttacaagg 1820

<210> 27

<211> 279

<212> PRT

<213> Homo sapiens

<400> 27

Met Glu Ala Val Val Asn Leu Tyr Gln Glu Val Met Lys His Ala Asp

1 5 10 15

Pro Arg Ile Gln Gly Tyr Pro Leu Met Gly Ser Pro Leu Leu Met Thr

20 25 30

Ser Ile Leu Leu Thr Tyr Val Tyr Phe Val Leu Ser Leu Gly Pro Arg

35 40 45

Ile Met Ala Asn Arg Lys Pro Phe Gln Leu Arg Gly Phe Met Ile Val

[illegible]

215



230

240

100

250

255

260

265

270

275

<211> 1472

⟨213⟩ Homo sapiens

<221> CDS

<400> 28

tgctccctcc gagcgctccg ccgttgccccg cctggccccct acggagtcct tagccagg 118

atg gag gct gtt gtg aac ttg tac caa gag gtg atg aag cac gca gat 166
 Met Glu Ala Val Val Asn Leu Tyr Gln Glu Val Met Lys His Ala Asp
 1 5 10 15

ccc cgg atc cag ggc tac cct ctg atg ggg tcc ccc ttg cta atg acc 214
 Pro Arg Ile Gln Gly Tyr Pro Leu Met Gly Ser Pro Leu Leu Met Thr
 20 25 30

tcc att ctc ctg acc tac gtg tac ttc gtt ctc tca ctt ggg cct cgc 262
 Ser Ile Leu Leu Thr Tyr Val Tyr Phe Val Leu Ser Leu Gly Pro Arg
 35 40 45

atc atg gct aat cgg aag ccc ttc cag ctc cgt ggc ttc atg att gtc 310
 Ile Met Ala Asn Arg Lys Pro Phe Gln Leu Arg Gly Phe Met Ile Val
 50 55 60

tac aac ttc tca ctg gtg gca ctc tcc ctc tac att gtc tat gag ttc 358
 Tyr Asn Phe Ser Leu Val Ala Leu Ser Leu Tyr Ile Val Tyr Glu Phe
 65 70 75 80

ctg atg tcg ggc tgg ctg agc acc tat acc tgg cgc tgt gac cct gtg 406
 Leu Met Ser Gly Trp Leu Ser Thr Tyr Thr Trp Arg Cys Asp Pro Val
 85 90 95

gac tat tcc aac agc cct gag gca ctt agg atg gtt cgg gtg gcc tgg 454
 Asp Tyr Ser Asn Ser Pro Glu Ala Leu Arg Met Val Arg Val Ala Trp
 100 105 110

ctc ttc ctc ttc tcc aag ttc att gag ctg atg gac aca gtg atc ttt 502

Leu Phe Leu Phe Ser Lys Phe Ile Glu Leu Met Asp Thr Val Ile Phe

115

120

125

att ctc cga aag aaa gac ggg cag gtg acc ttc cta cat gtc ttc cat 550

Ile Leu Arg Lys Lys Asp Gly Gln Val Thr Phe Leu His Val Phe His

130

135

140

cac tct gtg ctt ccc tgg agc tgg tgg tgg ggg gta aag att gcc ccg 598

His Ser Val Leu Pro Trp Ser Trp Trp Trp Gly Val Lys Ile Ala Pro

145

150

155

160

gga gga atg ggc tct ttc cat gcc atg ata aac tct tcc gtg cat gtc 646

Gly Gly Met Gly Ser Phe His Ala Met Ile Asn Ser Ser Val His Val

165

170

175

ata atg tac ctg tac tac gga tta tct gcc ttt ggc cct gtg gca caa 694

Ile Met Tyr Leu Tyr Tyr Gly Leu Ser Ala Phe Gly Pro Val Ala Gln

180

185

190

ccc tac ctt tgg tgg aaa aag cac atg aca gcc att cag ctg atc cag 742

Pro Tyr Leu Trp Trp Lys Lys His Met Thr Ala Ile Gln Leu Ile Gln

195

200

205

ttt gtc ctg gtc tca ctg cac atc tcc cag tac tac ttt atg tcc agc 790

Phe Val Leu Val Ser Leu His Ile Ser Gln Tyr Tyr Phe Met Ser Ser

210

215

220

tgt aac tac cag tac cca gtc att att cac ctc atc tgg atg tat ggc 838

Cys Asn Tyr Gln Tyr Pro Val Ile Ile His Leu Ile Trp Met Tyr Gly

225 230 235 240

acc atc ttc ttc atg ctg ttc tcc aac ttc tgg tat cac tct tat acc 886

Thr Ile Phe Phe Met Leu Phe Ser Asn Phe Trp Tyr His Ser Tyr Thr

245 250 255

aag ggc aag cgg ctg ccc cgt gca ctt cag caa aat gga gct cca ggt 934

Lys Gly Lys Arg Leu Pro Arg Ala Leu Gln Gln Asn Gly Ala Pro Gly

260 265 270

att gcc aag gtc aag gcc aac tgagaagcat ggcctagata ggcgcccacc 985

Ile Ala Lys Val Lys Ala Asn

275

taagtgcctc aggactgcac cttagggcag tgtccgtcag tgccctctcc acctacacct 1045

gtgaccaagg cttatgtggt caggactgag caggggactg gccctccctt cccacagct 1105

gctctacagg gaccacggct ttggttcctc acccacttcc cccggggcagc tccaggggatg 1165

tggcctcatt gctgtctgcc actccagagc tgggggctaa aagggtgta cagttatttc 1225

cccctccctg ccttaaaact tgggagagga gcactcaggg ctggccccac aaagggtctc 1285

gtggcctttt tcctcacaca gaagagggtca gcaataatgt cactgtggac ccagtctcac 1345

tcctccaccc cacacactga agcagtagct tctgggccaa aggtcagggt gggcgggggc 1405

ctgggaatac agcctgtgga ggctgcttac tcaacttggtg tcttaattaa aagtgcacaga 1465

ggaaacc 1472

<210> 29

<211> 137

<212> PRT

<213> Homo sapiens

<400> 29

Met Gly Phe Gly Ala Thr Leu Ala Val Gly Leu Thr Ile Phe Val Leu
1 5 10 15

Ser Val Val Thr Ile Ile Ile Cys Phe Thr Cys Ser Cys Cys Cys Leu
20 25 30

Tyr Lys Thr Cys Arg Arg Pro Arg Pro Val Val Thr Thr Thr Thr Ser
35 40 45

Thr Thr Val Val His Ala Pro Tyr Pro Gln Pro Pro Ser Val Pro Pro
50 55 60

Ser Tyr Pro Gly Pro Ser Tyr Gln Gly Tyr His Thr Met Pro Pro Gln
65 70 75 80

Pro Gly Met Pro Ala Ala Pro Tyr Pro Met Gln Tyr Pro Pro Pro Tyr
85 90 95

Pro Ala Gln Pro Met Gly Pro Pro Ala Tyr His Glu Thr Leu Ala Gly

100

105

110

Gly Ala Ala Ala Pro Tyr Pro Ala Ser Gln Pro Pro Tyr Asn Pro Ala

115

120

125

Tyr Met Asp Ala Pro Lys Ala Ala Leu

130

135

<210> 30

<211> 1788

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (145).. (555)

<400> 30

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ggaaattgaa actgagtggc ccacgatggg aagaggggaa agcccagggg tacaggaggc 120

ctctgggtga aggcagaggc taac atg ggg ttc gga gcg acc ttg gcc gtt 171

Met Gly Phe Gly Ala Thr Leu Ala Val

1

5

ggc ctg acc atc ttt gtg ctg tct gtc gtc act atc atc atc tgc ttc 219

Gly Leu Thr Ile Phe Val Leu Ser Val Val Thr Ile Ile Ile Cys Phe

10 15 20 25

acc tgc tcc tgc tgc tgc ctt tac aag acg tgc cgc cga cca cgt ccg 267

Thr Cys Ser Cys Cys Cys Leu Tyr Lys Thr Cys Arg Arg Pro Arg Pro

30 35 40

gtt gtc acc acc acc aca tcc acc act gtg gtg cat gcc cct tat cct 315

Val Val Thr Thr Thr Thr Ser Thr Thr Val Val His Ala Pro Tyr Pro

45 50 55

cag cct cca agt gtg ccg ccc agc tac cct gga cca agc tac cag ggc 363

Gln Pro Pro Ser Val Pro Pro Ser Tyr Pro Gly Pro Ser Tyr Gln Gly

60 65 70

tac cac acc atg ccg cct cag cca ggg atg cca gca gca ccc tac cca 411

Tyr His Thr Met Pro Pro Gln Pro Gly Met Pro Ala Ala Pro Tyr Pro

75 80 85

atg cag tac cca cca cct tac cca gcc cag ccc atg ggc cca ccg gcc 459

Met Gln Tyr Pro Pro Pro Tyr Pro Ala Gln Pro Met Gly Pro Pro Ala

90 95 100 105

tac cac gag acc ctg gct gga gga gca gcc gcg ccc tac ccc gcc agc 507

Tyr His Glu Thr Leu Ala Gly Gly Ala Ala Ala Pro Tyr Pro Ala Ser

110 115 120

cag cct cct tac aac ccg gcc tac atg gat gcc ccg aag gcg gcc ctc 555

Gln Pro Pro Tyr Asn Pro Ala Tyr Met Asp Ala Pro Lys Ala Ala Leu

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tgagtccttg ctccccgaca ccagcctcat ggaatatgca acaactcctg taccgccagt 1575

cacggtgttc tggcagcagg gacacctggg ccaatgggcc atctggacca aaggtgggggt 1635

gtggggccct ggatggcagc tctggcccag acatgaatac ctctgtgttc tctccctct 1695

attactgttt caccagagct gtcttagctc aaatctgttg tgtttctgag tctagggctc 1755

gtacacttgt ttataataaa tgcaatcggt tgg 1788

<210> 31

<211> 118

<212> PRT

⟨213⟩ Homo sapiens

<400> 31

Met Gly Phe Gly Ala Thr Leu Ala Val Gly Leu Thr Ile Phe Val Leu

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Ser Val Val Thr Ile Ile Ile Cys Phe Thr Cys Ser Cys Cys Cys Leu

20 25 30

Tyr Lys Thr Cys Arg Arg Pro Arg Pro Val Val Thr Thr Thr Thr Ser

ggaggcctct ggggtgaaggc agaggctaac atg ggg ttc gga gcg acc ttg gcc 114

Met Gly Phe Gly Ala Thr Leu Ala

1

5

gtt ggc ctg acc atc ttt gtg ctg tct gtc gtc act atc atc atc tgc 162

Val Gly Leu Thr Ile Phe Val Leu Ser Val Val Thr Ile Ile Ile Cys

10

15

20

ttc acc tgc tcc tgc tgc tgc ctt tac aag acg tgc cgc cga cca cgt 210

Phe Thr Cys Ser Cys Cys Cys Leu Tyr Lys Thr Cys Arg Arg Pro Arg

25

30

35

40

ccg gtt gtc acc acc acc aca tcc acc act gtg gtg cat gcc cct tat 258

Pro Val Val Thr Thr Thr Thr Ser Thr Thr Val Val His Ala Pro Tyr

45

50

55

cct cag cct cca agt gtg ccg ccc agc tac cct gga cca agc tac cag 306

Pro Gln Pro Pro Ser Val Pro Pro Ser Tyr Pro Gly Pro Ser Tyr Gln

60

65

70

ggc tac cac acc atg ccg cct cag cca ggg atg cca gca gca ccc tac 354

Gly Tyr His Thr Met Pro Pro Gln Pro Gly Met Pro Ala Ala Pro Tyr

75

80

85

cca atg cag tac cca cca cct tac cca gcc cag ccc atg ggc cca ccg 402

Pro Met Gln Tyr Pro Pro Pro Tyr Pro Ala Gln Pro Met Gly Pro Pro

90

95

100

gcc tac cac gag acc ctg gct ggt gag tgc ccc tgc caa ctc 444

Ala Tyr His Glu Thr Leu Ala Gly Glu Cys Pro Cys Gln Leu

105

110

115

tagccctgcc cgacttcccg agtctctgcc agcatccctc gggcacccat cccaaactac 504

atcactcaac aggcctctgc ccctttctgc ttgcctgcca ctacacaggc agcccacat 564

gctcacagcc aaccagggtc ctctctgctt tcaggaggag cagccgcgcc ctaccccgcc 624

agccagcctc cttacaaccc ggcctacatg gatgccccga aggcggccct ctgagcattc 684

cctggcctct ctggetgcca cttggttatg ttgtgtgtgt gcgtgagtgg tgtgcaggcg 744

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cccctggggt gtggaggga attggctcag agatggacaa cctggcaact gtgagtcct 1644

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tggatggcag ctctggccca gacatgaata cctcgtgttc ctctccctc tattactgtt 1824

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<210> 33

<211> 168

<212> PRT

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(The following information was obtained from the records of the Department of Health, Education and Welfare, Washington, D.C., and the National Archives and Records Administration, College Park, Md.)

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[illegible]

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Met Asn Ser Lys Gly Gln Tyr Pro Thr Gln Pro Thr Tyr Pro

gtg cag cct cct ggg aat cca gta tac cct cag acc ttg cat ctt cct 159

15 20 25 30

88/735

Gln Ala Pro Pro Tyr Thr Asp Ala Pro Pro Ala Tyr Ser Glu Leu Tyr
35 40 45

cgt ccg agc ttt gtg cac cca ggg gct gcc aca gtc ccc acc atg tca 255
Arg Pro Ser Phe Val His Pro Gly Ala Ala Thr Val Pro Thr Met Ser
50 55 60

gcc gca ttt cct gga gcc tct ctg tat ctt ccc atg gcc cag tct gtg 303
Ala Ala Phe Pro Gly Ala Ser Leu Tyr Leu Pro Met Ala Gln Ser Val
65 70 75

gct gtt ggg cct tta ggt tcc aca atc ccc atg gct tat tat cca gtc 351
Ala Val Gly Pro Leu Gly Ser Thr Ile Pro Met Ala Tyr Tyr Pro Val
80 85 90

ggt ccc atc tat cca cct ggc tcc aca gtg ctg gtg gaa gga ggg tat 399
Gly Pro Ile Tyr Pro Pro Gly Ser Thr Val Leu Val Glu Gly Gly Tyr
95 100 105 110

gat gca ggt gcc aga ttt gga gct ggg gct act gct ggc aac att cct 447
Asp Ala Gly Ala Arg Phe Gly Ala Gly Ala Thr Ala Gly Asn Ile Pro
115 120 125

cct cca cct cct gga tgc cct ccc aat gct gct cag ctt gca gtc atg 495
Pro Pro Pro Pro Gly Cys Pro Pro Asn Ala Ala Gln Leu Ala Val Met
130 135 140

cag gga gcc aac gtc ctc gta act cag cgg aag ggg aac ttc ttc atg 543
Gln Gly Ala Asn Val Leu Val Thr Gln Arg Lys Gly Asn Phe Phe Met
89/735

145

150

155

ggt ggt tca gat ggt ggc tac acc atc tgg tgaggaaacca aggccacctc 593

Gly Gly Ser Asp Gly Gly Tyr Thr Ile Trp

160

165

tgtgccggga aagacatcac ataccttcag cacttctcac aatgtaactg ctttagtcat 653

attaacctga agttgcagtt tagacacatg ttgttgggggt gtctttctgg tgcccaaact 713

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<210> 35

<211> 455

<212> PRT

<213> Homo sapiens

<400> 35

Met Ser Phe Leu Ile Asp Ser Ser Ile Met Ile Thr Ser Gln Ile Leu

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Phe Phe Gly Phe Gly Trp Leu Phe Phe Met Arg Gln Leu Phe Lys Asp

20 25 30

Tyr Glu Ile Arg Gln Tyr Val Val Gln Val Ile Phe Ser Val Thr Phe

35 40 45

Ala Phe Ser Cys Thr Met Phe Glu Leu Ile Ile Phe Glu Ile Leu Gly

50 55 60

Val Leu Asn Ser Ser Ser Arg Tyr Phe His Trp Lys Met Asn Leu Cys

65 70 75 80

Val Ile Leu Leu Ile Leu Val Phe Met Val Pro Phe Tyr Ile Gly Tyr

85 90 95

Phe Ile Val Ser Asn Ile Arg Leu Leu His Lys Gln Arg Leu Leu Phe

100 105 110

Ser Cys Leu Leu Trp Leu Thr Phe Met Tyr Phe Phe Trp Lys Leu Gly

115 120 125

Asp Pro Phe Pro Ile Leu Ser Pro Lys His Gly Ile Leu Ser Ile Glu

130 135 140

Gln Leu Ile Ser Arg Val Gly Val Ile Gly Val Thr Leu Met Ala Leu

145 150 155 160

<210> 36

<211> 1903

<212> DNA

<213> Homo sapiens

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<222> (116).. (1480)

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tgctgtggcc tcggggagtg ggaagtggag gcaggagcct tccttacact tcgcc atg 118

Met

1

agt ttc ctc atc gac tcc agc atc atg att acc tcc cag ata cta ttt 166

Ser Phe Leu Ile Asp Ser Ser Ile Met Ile Thr Ser Gln Ile Leu Phe

5

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ttt gga ttt ggg tgg ctt ttc ttc atg cgc caa ttg ttt aaa gac tat 214

Phe Gly Phe Gly Trp Leu Phe Phe Met Arg Gln Leu Phe Lys Asp Tyr

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25

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gag ata cgt cag tat gtt gta cag gtg atc ttc tcc gtg acg ttt gca 262

Glu Ile Arg Gln Tyr Val Val Gln Val Ile Phe Ser Val Thr Phe Ala

35

40

45

ttt tct tgc acc atg ttt gag ctc atc atc ttt gaa atc tta gga gta 310

Phe Ser Cys Thr Met Phe Glu Leu Ile Ile Phe Glu Ile Leu Gly Val

50

55

60

65

ttg aat agc agc tcc cgt tat ttt cac tgg aaa atg aac ctg tgt gta 358

Leu Asn Ser Ser Ser Arg Tyr Phe His Trp Lys Met Asn Leu Cys Val

70

75

80

att ctg ctg atc ctg gtt ttc atg gtg cct ttt tac att ggc tat ttt 406

Ile Leu Leu Ile Leu Val Phe Met Val Pro Phe Tyr Ile Gly Tyr Phe

85

90

95

att gtg agc aat atc cga cta ctg cat aaa caa cga ctg ctt ttt tcc 454

Ile Val Ser Asn Ile Arg Leu Leu His Lys Gln Arg Leu Leu Phe Ser

100

105

110

tgt ctc tta tgg ctg acc ttt atg tat ttc ttc tgg aaa cta gga gat 502

Cys Leu Leu Trp Leu Thr Phe Met Tyr Phe Phe Trp Lys Leu Gly Asp

115

120

125

ccc ttt ccc att ctc agc cca aaa cat ggg atc tta tcc ata gaa cag 550

Pro Phe Pro Ile Leu Ser Pro Lys His Gly Ile Leu Ser Ile Glu Gln

130

135

140

145

ctc atc agc cgg gtt ggt gtg att gga gtg act ctc atg gct ctt ctt 598

Leu Ile Ser Arg Val Gly Val Ile Gly Val Thr Leu Met Ala Leu Leu

150

155

160

tct gga ttt ggt gct gtc aac tgc cca tac act tac atg tct tac ttc 646

Ser Gly Phe Gly Ala Val Asn Cys Pro Tyr Thr Tyr Met Ser Tyr Phe

165	170	175	
ctc agg aat gtg act gac acg gat att cta gcc ctg gaa cgg cga ctg			694
Leu Arg Asn Val Thr Asp Thr Asp Ile Leu Ala Leu Glu Arg Arg Leu			
180	185	190	
ctg caa acc atg gat atg atc ata agc aaa aag aaa agg atg gca atg			742
Leu Gln Thr Met Asp Met Ile Ile Ser Lys Lys Lys Arg Met Ala Met			
195	200	205	
gca cgg aga aca atg ttc cag aag ggg gaa gtg cat aac aaa cca tca			790
Ala Arg Arg Thr Met Phe Gln Lys Gly Glu Val His Asn Lys Pro Ser			
210	215	220	225
ggt ttc tgg gga atg ata aaa agt gtt acc act tca gca tca gga agt			838
Gly Phe Trp Gly Met Ile Lys Ser Val Thr Thr Ser Ala Ser Gly Ser			
230	235	240	
gaa aat ctt act ctt att caa cag gaa gtg gat gct ttg gaa gaa tta			886
Glu Asn Leu Thr Leu Ile Gln Gln Glu Val Asp Ala Leu Glu Glu Leu			
245	250	255	
agc agg cag ctt ttt ctg gaa aca gct gat cta tat gct acc aag gag			934
Ser Arg Gln Leu Phe Leu Glu Thr Ala Asp Leu Tyr Ala Thr Lys Glu			
260	265	270	
aga ata gaa tac tcc aaa acc ttc aag ggg aaa tat ttt aat ttt ctt			982
Arg Ile Glu Tyr Ser Lys Thr Phe Lys Gly Lys Tyr Phe Asn Phe Leu			
275	280	285	

ggt tac ttt ttc tct att tac tgt gtt tgg aaa att ttc atg gct acc 1030
 Gly Tyr Phe Phe Ser Ile Tyr Cys Val Trp Lys Ile Phe Met Ala Thr
 290 295 300 305

atc aat att gtt ttt gat cga gtt ggg aaa acg gat cct gtc aca aga 1078
 Ile Asn Ile Val Phe Asp Arg Val Gly Lys Thr Asp Pro Val Thr Arg
 310 315 320

ggc att gag atc act gtg aat tat ctg gga atc caa ttt gat gtg aag 1126
 Gly Ile Glu Ile Thr Val Asn Tyr Leu Gly Ile Gln Phe Asp Val Lys
 325 330 335

ttt tgg tcc caa cac att tcc ttc att ctt gtt gga ata atc atc gtc 1174
 Phe Trp Ser Gln His Ile Ser Phe Ile Leu Val Gly Ile Ile Ile Val
 340 345 350

aca tcc atc aga gga ttg ctg atc act ctt acc aag ttc ttt tat gcc 1222
 Thr Ser Ile Arg Gly Leu Leu Ile Thr Leu Thr Lys Phe Phe Tyr Ala
 355 360 365

atc tct agc agt aag tcc tcc aat gtc att gtc ctg cta tta gca cag 1270
 Ile Ser Ser Ser Lys Ser Ser Asn Val Ile Val Leu Leu Leu Ala Gln
 370 375 380 385

ata atg ggc atg tac ttt gtc tcc tct gtg ctg ctg atc cga atg agt 1318
 Ile Met Gly Met Tyr Phe Val Ser Ser Val Leu Leu Ile Arg Met Ser
 390 395 400

atg cct tta gaa tac cgc acc ata atc act gaa gtc ctt gga gaa ctg 1366

Met Pro Leu Glu Tyr Arg Thr Ile Ile Thr Glu Val Leu Gly Glu Leu

405

410

415

cag ttc aac ttc tat cac cgt tgg ttt gat gtg atc ttc ctg gtc agc 1414

Gln Phe Asn Phe Tyr His Arg Trp Phe Asp Val Ile Phe Leu Val Ser

420

425

430

gct ctc tct agc ata ctc ttc ctc tat ttg gct cac aaa cag gca cca 1462

Ala Leu Ser Ser Ile Leu Phe Leu Tyr Leu Ala His Lys Gln Ala Pro

435

440

445

gag aag caa atg gca cct tgaacttaag cctactacag actgttagag 1510

Glu Lys Gln Met Ala Pro

450

455

gccagtgggtt tcaaaattta gatataagag gggggaaaaa tggaaccagg gcctgacatt 1570

ttataaaca acaaaatgct atggtagcat tttcacctt catagcatac tccttccccg 1630

tcaggtgata ctatgaccat gagtagcatc agccagaaca tgagagggag aactaactca 1690

agacaatact cagcagagag catcccgtgt ggatatgagg ctggtgtaga ggcggagagg 1750

agccaagaaa ctaaagggtga aaaatacact ggaactctgg ggcaagacat gtctatggta 1810

gctgagccaa acacgtagga tttccgtttt aaggttcaca tggaagaggt tatagctttg 1870

ccttgagatt gactcattaa aatcagagac tgt

1903

<210> 37

<211> 322

<212> PRT

<213> Homo sapiens

<400> 37

Met Ser Ser Leu Gly Gly Gly Ser Gln Asp Ala Gly Gly Ser Ser Ser

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5

10

15

Ser Ser Thr Asn Gly Ser Gly Gly Ser Gly Ser Ser Gly Pro Lys Ala

20

25

30

Gly Ala Ala Asp Lys Ser Ala Val Val Ala Ala Ala Ala Pro Ala Ser

35

40

45

Val Ala Asp Asp Thr Pro Pro Pro Glu Arg Arg Asn Lys Ser Gly Ile

50

55

60

Ile Ser Glu Pro Leu Asn Lys Ser Leu Arg Arg Ser Arg Pro Leu Ser

65

70

75

80

His Tyr Ser Ser Phe Gly Ser Ser Gly Gly Ser Gly Gly Gly Ser Met

85

90

95

Met Gly Gly Glu Ser Ala Asp Lys Ala Thr Ala Ala Ala Ala Ala Ala

100

105

110

Ile Asn Cys Glu Gln Cys Ser Ser Cys Arg Asn Arg Lys Thr Gly His
275 280 285

Gln Ile Cys Lys Phe Arg Lys Cys Glu Glu Leu Lys Lys Lys Pro Ser
290 295 300

Ala Ala Leu Glu Lys Val Met Leu Pro Thr Gly Ala Ala Phe Arg Trp
305 310 315 320

Phe Gln

<210> 38

<211> 1448

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (292)..(1257)

<400> 38

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tcggagagcc gagtgaagac atttcacct ggacacctga ccatgtgcct gccctgagca 180

gcgaggcccca ccaggcatct ctgttgtggg cagcaggggc aggtcctggt ctgtggaccc 240

tccggcagttg gcaggctccc tctgcagtgg ggtctggggcc tcggccccac c atg tcg 297

Met Ser

1

agc ctc ggc ggt ggc tcc cag gat gcc ggc ggc agt agc agc agc agc 345

Ser Leu Gly Gly Gly Ser Gln Asp Ala Gly Gly Ser Ser Ser Ser Ser

5

10

15

acc aat ggc agc ggt ggc agt ggc agc agt ggc cca aag gca gga gca 393

Thr Asn Gly Ser Gly Gly Ser Gly Ser Ser Gly Pro Lys Ala Gly Ala

20

25

30

gca gac aag agt gca gtg gtg gct gcc gcc gca cca gcc tca gtg gca 441

Ala Asp Lys Ser Ala Val Val Ala Ala Ala Ala Pro Ala Ser Val Ala

35

40

45

50

gat gac aca cca ccc ccc gag cgt cgg aac aag agc ggt atc atc agt 489

Asp Asp Thr Pro Pro Pro Glu Arg Arg Asn Lys Ser Gly Ile Ile Ser

55

60

65

gag ccc ctc aac aag agc ctg cgc cgc tcc cgc ccg ctc tcc cac tac 537

Glu Pro Leu Asn Lys Ser Leu Arg Arg Ser Arg Pro Leu Ser His Tyr

70

75

80

tct tct ttt ggc agc agt ggt ggt agt ggc ggt ggc agc atg atg ggc 585

Ser Ser Phe Gly Ser Ser Gly Gly Ser Gly Gly Gly Ser Met Met Gly

85

90

95

gga gag tct gct gac aag gcc act gcg gct gca gcc gct gcc tcc ctg 633

Gly Glu Ser Ala Asp Lys Ala Thr Ala Ala Ala Ala Ala Ala Ser Leu

100

105

110

ttg gcc aat ggg cat gac ctg gcg gcg gcc atg gcg gtg gac aaa agc 681

Leu Ala Asn Gly His Asp Leu Ala Ala Ala Met Ala Val Asp Lys Ser

115

120

125

130

aac cct acc tca aag cac aaa agt ggt gct gtg gcc agc ctg ctg agc 729

Asn Pro Thr Ser Lys His Lys Ser Gly Ala Val Ala Ser Leu Leu Ser

135

140

145

aag gca gag cgg gcc acg gag ctg gca gcc gag gga cag ctg acg ctg 777

Lys Ala Glu Arg Ala Thr Glu Leu Ala Ala Glu Gly Gln Leu Thr Leu

150

155

160

cag cag ttt gcg cag tcc aca gag atg ctg aag cgc gtg gtg cag gag 825

Gln Gln Phe Ala Gln Ser Thr Glu Met Leu Lys Arg Val Val Gln Glu

165

170

175

cat ctc ccg ctg atg agc gag gcg ggt gct ggc ctg cct gac atg gag 873

His Leu Pro Leu Met Ser Glu Ala Gly Ala Gly Leu Pro Asp Met Glu

180

185

190

gct gtg gca ggt gcc gaa gcc ctc aat ggc cag tcc gac ttc ccc tac 921

Ala Val Ala Gly Ala Glu Ala Leu Asn Gly Gln Ser Asp Phe Pro Tyr

195

200

205

210

ctg ggc gct ttc ccc atc aac cca ggc ctc ttc att atg acc ccg gca 969

Leu Gly Ala Phe Pro Ile Asn Pro Gly Leu Phe Ile Met Thr Pro Ala

215

220

225

ggt gtg ttc ctg gcc gag agc gcg ctg cac atg gcg ggc ctg gct gag 1017

Gly Val Phe Leu Ala Glu Ser Ala Leu His Met Ala Gly Leu Ala Glu

230

235

240

tac ccc atg cag gga gag ctg gcc tct gcc atc agc tcc ggc aag aag 1065

Tyr Pro Met Gln Gly Glu Leu Ala Ser Ala Ile Ser Ser Gly Lys Lys

245

250

255

aag cgg aaa cgc tgc ggc atg tgc gcg ccc tgc cgg cgg cgc atc aac 1113

Lys Arg Lys Arg Cys Gly Met Cys Ala Pro Cys Arg Arg Arg Ile Asn

260

265

270

tgc gag cag tgc agc agt tgt agg aat cga aag act ggc cat cag att 1161

Cys Glu Gln Cys Ser Ser Cys Arg Asn Arg Lys Thr Gly His Gln Ile

275

280

285

290

tgc aaa ttc aga aaa tgt gag gaa ctc aaa aag aag cct tcc gct gct 1209

Cys Lys Phe Arg Lys Cys Glu Glu Leu Lys Lys Lys Pro Ser Ala Ala

295

300

305

ctg gag aag gtg atg ctt ccg acg gga gcc gcc ttc cgg tgg ttt cag 1257

Leu Glu Lys Val Met Leu Pro Thr Gly Ala Ala Phe Arg Trp Phe Gln

310

315

320

tgacggcggc ggaacccaaa gctgccctct ccgtgcaatg tcaactgctcg tgtggtctcc 1317

agcaagggat tcgggcgaag acaaacggat gcacccgtct ttagaaccaa aaatattctc 1377

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gtccctagca t 1448

<210> 39

<211> 313

<212> PRT

<213> Homo sapiens

<400> 39

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20 25 30

Pro Asn Thr Leu Ser Phe Arg Cys Ser Leu Ala Asp Phe Gln Ile Glu

35 40 45

Lys Lys Ile Gly Arg Gly Gln Phe Ser Glu Val Tyr Lys Ala Thr Cys

50 55 60

Leu Leu Asp Arg Lys Thr Val Ala Leu Lys Lys Val Gln Ile Phe Glu

65 70 75 80

225 230 235 240

Ala Ala Leu Gln Ser Pro Phe Tyr Gly Asp Lys Met Asn Leu Phe Ser

245 250 255

Leu Cys Gln Lys Ile Glu Gln Cys Asp Tyr Pro Pro Leu Pro Gly Glu

260 265 270

His Tyr Ser Glu Lys Leu Arg Glu Leu Val Ser Met Cys Ile Cys Pro

275 280 285

Asp Pro His Gln Arg Pro Asp Ile Gly Tyr Val His Gln Val Ala Lys

290 295 300

Gln Met His Ile Trp Met Ser Ser Thr

305 310

<210> 40

<211> 1597

<212> DNA

<213> Homo sapiens

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<222> (153).. (1091)

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ccgttcgtgc cctcgtgagg ctggcatgca gg atg gca gga cag ccc ggc cac 173

Met Ala Gly Gln Pro Gly His

1

5

atg ccc cat gga ggg agt tcc aac aac ctc tgc cac acc ctg ggg cct 221

Met Pro His Gly Gly Ser Ser Asn Asn Leu Cys His Thr Leu Gly Pro

10

15

20

gtg cat cct cct gac cca cag agg cat ccc aac acg ctg tct ttt cgc 269

Val His Pro Pro Asp Pro Gln Arg His Pro Asn Thr Leu Ser Phe Arg

25

30

35

tgc tcg ctg gcg gac ttc cag atc gaa aag aag ata ggc cga gga cag 317

Cys Ser Leu Ala Asp Phe Gln Ile Glu Lys Lys Ile Gly Arg Gly Gln

40

45

50

55

ttc agc gag gtg tac aag gcc acc tgc ctg ctg gac agg aag aca gtg 365

Phe Ser Glu Val Tyr Lys Ala Thr Cys Leu Leu Asp Arg Lys Thr Val

60

65

70

gct ctg aag aag gtg cag atc ttt gag atg atg gac gcc aag gcg agg 413

Ala Leu Lys Lys Val Gln Ile Phe Glu Met Met Asp Ala Lys Ala Arg

75

80

85

cag gac tgt gtc aag gag atc ggc ctc ttg aag caa ctg aac cac cca 461

Gln Asp Cys Val Lys Glu Ile Gly Leu Leu Lys Gln Leu Asn His Pro

ccg gag agg atc cat gag aac ggc tac aac ttc aag tcc gac atc tgg 845

Pro Glu Arg Ile His Glu Asn Gly Tyr Asn Phe Lys Ser Asp Ile Trp

220

225

230

tcc ttg ggc tgt ctg ctg tac gag atg gca gcc ctc cag agc ccc ttc 893

Ser Leu Gly Cys Leu Leu Tyr Glu Met Ala Ala Leu Gln Ser Pro Phe

235

240

245

tat gga gat aag atg aat ctc ttc tcc ctg tgc cag aag atc gag cag 941

Tyr Gly Asp Lys Met Asn Leu Phe Ser Leu Cys Gln Lys Ile Glu Gln

250

255

260

tgt gac tac ccc cca ctc ccc ggg gag cac tac tcc gag aag tta cga 989

Cys Asp Tyr Pro Pro Leu Pro Gly Glu His Tyr Ser Glu Lys Leu Arg

265

270

275

gaa ctg gtc agc atg tgc atc tgc cct gac ccc cac cag aga cct gac 1037

Glu Leu Val Ser Met Cys Ile Cys Pro Asp Pro His Gln Arg Pro Asp

280

285

290

295

atc gga tac gtg cac cag gtg gcc aag cag atg cac atc tgg atg tcc 1085

Ile Gly Tyr Val His Gln Val Ala Lys Gln Met His Ile Trp Met Ser

300

305

310

agc acc tgagcgtgga tgcaccgtgc cttatcaaag ccagcaccac tttgccttac 1141

Ser Thr

ttgagtcgtc ttctcttcga gtggccacct ggtagcctag aacagctaag accacagggt 1201

[illegible][illegible][illegible][illegible][illegible][illegible][illegible][illegible]

$\frac{1}{\sqrt{2}} \left(\begin{array}{c} |1\rangle \\ |0\rangle \end{array} \right) = \frac{1}{\sqrt{2}} \left(\begin{array}{c} |1\rangle \\ |0\rangle \end{array} \right)$

[illegible][illegible][illegible][illegible][illegible][illegible][illegible][illegible]

..

35

40

45

Pro Ser Pro Tyr Gly Gln Pro Gly Tyr Pro His Gly Pro Ser Pro Tyr

50

55

60

Pro Gln Gly Gly Tyr Pro Gln Gly Pro Tyr Pro Gln Gly Gly Tyr Pro

65

70

75

80

Gln Gly Pro Tyr Pro Gln Glu Gly Tyr Pro Gln Gly Pro Tyr Pro Gln

85

90

95

Gly Gly Tyr Pro Gln Gly Pro Tyr Pro Gln Ser Pro Phe Pro Pro Asn

100

105

110

Pro Tyr Gly Gln Pro Gln Val Phe Pro Gly Gln Asp Pro Asp Ser Pro

115

120

125

Gln His Gly Asn Tyr Gln Glu Glu Gly Pro Pro Ser Tyr Tyr Asp Asn

130

135

140

Gln Asp Phe Pro Ala Thr Asn Trp Asp Asp Lys Ser Ile Arg Gln Ala

145

150

155

160

Phe Ile Arg Lys Val Phe Leu Val Leu Thr Leu Gln Leu Ser Val Thr

165

170

175

Leu Ser Thr Val Ser Val Phe Thr Phe Val Ala Glu Val Lys Gly Phe

180

185

190

Val Arg Glu Asn Val Trp Thr Tyr Tyr Val Ser Tyr Ala Val Phe Phe
195 200 205

Ile Ser Leu Ile Val Leu Ser Cys Cys Gly Asp Phe Arg Arg Lys His
210 215 220

Pro Trp Asn Leu Val Ala Leu Ser Val Leu Thr Ala Ser Leu Ser Tyr
225 230 235 240

Met Val Gly Met Ile Ala Ser Phe Tyr Asn Thr Glu Ala Val Ile Met
245 250 255

Ala Val Gly Ile Thr Thr Ala Val Cys Phe Thr Val Val Ile Phe Ser
260 265 270

Met Gln Thr Arg Tyr Asp Phe Thr Ser Cys Met Gly Val Leu Leu Val
275 280 285

Ser Met Val Val Leu Phe Ile Phe Ala Ile Leu Cys Ile Phe Ile Arg
290 295 300

Asn Arg Ile Leu Glu Ile Val Tyr Ala Ser Leu Gly Ala Leu Leu Phe
305 310 315 320

Thr Cys Phe Leu Ala Val Asp Thr Gln Leu Leu Leu Gly Asn Lys Gln
325 330 335

Leu Ser Leu Ser Pro Glu Glu Tyr Val Phe Ala Ala Leu Asn Leu Tyr
340 345 350

Pro Gln Pro Pro Met Pro Pro Tyr Ala Gln Pro Pro Tyr Pro Gly Ala

25 30 35 40

cct tac cca cag ccc cct ttc cag ccc tcc ccc tac ggt cag cca ggg 258

Pro Tyr Pro Gln Pro Pro Phe Gln Pro Ser Pro Tyr Gly Gln Pro Gly

45 50 55

tac ccc cat ggc ccc agc ccc tac ccc caa ggg ggc tac cca cag ggt 306

Tyr Pro His Gly Pro Ser Pro Tyr Pro Gln Gly Gly Tyr Pro Gln Gly

60 65 70

ccc tac ccc caa ggg ggc tac cca cag ggc ccc tac cca caa gag ggc 354

Pro Tyr Pro Gln Gly Gly Tyr Pro Gln Gly Pro Tyr Pro Gln Glu Gly

75 80 85

tac cca cag ggc ccc tac ccc caa ggg ggc tac ccc cag ggg cca tat 402

Tyr Pro Gln Gly Pro Tyr Pro Gln Gly Gly Tyr Pro Gln Gly Pro Tyr

90 95 100

ccc cag agc ccc ttc ccc ccc aac ccc tat gga cag cca cag gtc ttc 450

Pro Gln Ser Pro Phe Pro Pro Asn Pro Tyr Gly Gln Pro Gln Val Phe

105 110 115 120

cca gga caa gac cct gac tca ccc cag cat gga aac tac cag gag gag 498

Pro Gly Gln Asp Pro Asp Ser Pro Gln His Gly Asn Tyr Gln Glu Glu

125 130 135

ggt ccc cca tcc tac tat gac aac cag gac ttc cct gcc acc aac tgg 546

Gly Pro Pro Ser Tyr Tyr Asp Asn Gln Asp Phe Pro Ala Thr Asn Trp

140	145	150	
gat gac aag agc atc cga cag gcc ttc atc cgc aag gtg ttc cta gtg			594
Asp Asp Lys Ser Ile Arg Gln Ala Phe Ile Arg Lys Val Phe Leu Val			
155	160	165	
ctg acc ttg cag ctg tcg gtg acc ctg tcc acg gtg tct gtg ttc act			642
Leu Thr Leu Gln Leu Ser Val Thr Leu Ser Thr Val Ser Val Phe Thr			
170	175	180	
ttt gtt gcg gag gtg aag ggc ttt gtc cgg gag aat gtc tgg acc tac			690
Phe Val Ala Glu Val Lys Gly Phe Val Arg Glu Asn Val Trp Thr Tyr			
185	190	195	200
tat gtc tcc tat gct gtc ttc ttc atc tct ctc atc gtc ctc agc tgt			738
Tyr Val Ser Tyr Ala Val Phe Phe Ile Ser Leu Ile Val Leu Ser Cys			
205	210	215	
tgt ggg gac ttc cgg cga aag cac ccc tgg aac ctt gtt gca ctg tcg			786
Cys Gly Asp Phe Arg Arg Lys His Pro Trp Asn Leu Val Ala Leu Ser			
220	225	230	
gtc ctg acc gcc agc ctg tcg tac atg gtg ggg atg atc gcc agc ttc			834
Val Leu Thr Ala Ser Leu Ser Tyr Met Val Gly Met Ile Ala Ser Phe			
235	240	245	
tac aac acc gag gca gtc atc atg gcc gtg ggc atc acc aca gcc gtc			882
Tyr Asn Thr Glu Ala Val Ile Met Ala Val Gly Ile Thr Thr Ala Val			
250	255	260	

tgc ttc acc gtc gtc atc ttc tcc atg cag acc cgc tac gac ttc acc 930
 Cys Phe Thr Val Val Ile Phe Ser Met Gln Thr Arg Tyr Asp Phe Thr
 265 270 275 280

tca tgc atg ggc gtg ctc ctg gtg agc atg gtg gtg ctc ttc atc ttc 978
 Ser Cys Met Gly Val Leu Leu Val Ser Met Val Val Leu Phe Ile Phe
 285 290 295

gcc att ctc tgc atc ttc atc cgg aac cgc atc ctg gag atc gtg tac 1026
 Ala Ile Leu Cys Ile Phe Ile Arg Asn Arg Ile Leu Glu Ile Val Tyr
 300 305 310

gcc tca ctg ggc gct ctg ctc ttc acc tgc ttc ctc gca gtg gac acc 1074
 Ala Ser Leu Gly Ala Leu Leu Phe Thr Cys Phe Leu Ala Val Asp Thr
 315 320 325

cag ctg ctg ctg ggg aac aag cag ctg tcc ctg agc cca gaa gag tat 1122
 Gln Leu Leu Leu Gly Asn Lys Gln Leu Ser Leu Ser Pro Glu Glu Tyr
 330 335 340

gtg ttt gct gcg ctg aac ctg tac aca gac atc atc aac atc ttc ctg 1170
 Val Phe Ala Ala Leu Asn Leu Tyr Thr Asp Ile Ile Asn Ile Phe Leu
 345 350 355 360

tac atc ctc acc atc att ggc cgc gcc aag gag tagccgagct ccagctcgct 1223
 Tyr Ile Leu Thr Ile Ile Gly Arg Ala Lys Glu
 365 370

gtgcccgcgc aggtggcacg gctggcctgg accctgcccc tggcacggca gtgccagctg 1283

tacttccct ctctcttgtc cccaggcaca gcctagggaa aaggatgcct ctctccaacc 1343

ctcctgtatg tacactgcag atacttccat ttggaccgcg tgtggccaca gcatggcccc 1403

tttagtcctc cgcceccgc caaggggcag caaggccacg ttccgtgcc acctcctgtc 1463

tactcattgt tgcattgagcc ctgtctgccg gccacaccca gggactggggg gcagcaccag 1523

gtcccgggga gagggattga gccaaagaggt gaggggtgcac gtcttccctc ctgtcccage 1583

tccccagcct ggcgtagage acccctcccc tccccccac cccctggag tgctgccctc 1643

tggggacatg cggagtgggg gtcttataccc tgtgctgagc cctgagggca gagaggatgg 1703

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tgggatttgc tctctgcc 1781

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<212> PRT

<213> Homo sapiens

<400> 43

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10

15

Ser Ser Pro Pro Pro Lys Thr Glu Ala Ala Ser Asp Pro Gln His Pro

20

25

30

Ala Ala Ser Glu Gly Ala Ala Ala Ala Ala Ala Ser Pro Pro Leu Leu

35

40

45

Arg Cys Leu Val Leu Thr Gly Phe Gly Gly Tyr Asp Lys Val Lys Leu

50

55

60

Gln Ser Arg Pro Ala Ala Pro Pro Ala Pro Gly Pro Gly Gln Leu Thr

65

70

75

80

Leu Arg Leu Arg Ala Cys Gly Leu Asn Phe Ala Asp Leu Met Ala Arg

85

90

95

Gln Gly Leu Tyr Asp Arg Leu Pro Pro Leu Pro Val Thr Pro Gly Met

100

105

110

Glu Gly Ala Gly Val Val Ile Ala Val Gly Glu Gly Val Ser Asp Arg

115

120

125

Lys Ala Gly Asp Arg Val Met Val Leu Asn Arg Ser Gly Met Trp Gln

130

135

140

Glu Glu Val Thr Val Pro Ser Val Gln Thr Phe Leu Ile Pro Glu Ala

145

150

155

160

Met Thr Phe Glu Glu Ala Ala Ala Leu Leu Val Asn Tyr Ile Thr Ala

120/735

..

165

170

175

Tyr Met Val Leu Phe Asp Phe Gly Asn Leu Gln Pro Gly His Ser Val

180

185

190

Leu Val His Met Ala Ala Gly Gly Val Gly Met Ala Ala Val Gln Leu

195

200

205

Cys Arg Thr Val Glu Asn Val Thr Val Phe Gly Thr Ala Ser Ala Ser

210

215

220

Lys His Glu Ala Leu Lys Glu Asn Gly Val Thr His Pro Ile Asp Tyr

225

230

235

240

His Thr Thr Asp Tyr Val Asp Glu Ile Lys Lys Ile Ser Pro Lys Gly

245

250

255

Val Asp Ile Val Met Asp Pro Leu Gly Gly Ser Asp Thr Ala Lys Gly

260

265

270

Tyr Asn Leu Leu Lys Pro Met Gly Lys Val Val Thr Tyr Gly Met Ala

275

280

285

Asn Leu Leu Thr Gly Pro Lys Arg Asn Leu Met Ala Leu Ala Arg Thr

290

295

300

Trp Trp Asn Gln Phe Ser Val Thr Ala Leu Gln Leu Leu Gln Ala Asn

305

310

315

320

.. .. .

Arg Ala Val Cys Gly Phe His Leu Gly Tyr Leu Asp Gly Glu Val Glu

325

330

335

Leu Val Ser Gly Val Val Ala Arg Leu Leu Ala Leu Tyr Asn Gln Gly

340

345

350

His Ile Lys Pro His Ile Asp Ser Val Trp Pro Phe Glu Lys Val Ala

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Asp Ala Met Lys Gln Met Gln Glu Lys Lys Asn Val Gly Lys Val Leu

370

375

380

Leu Val Pro Gly Pro Glu Lys Glu Asn

385

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<211> 2396

<212> DNA

<213> Homo sapiens

<220>

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Met Ser Asp

gag aga gag gta gcc gag gca gcg acc ggg gaa gac gcc tct tcg ccg 106
 Glu Arg Glu Val Ala Glu Ala Ala Thr Gly Glu Asp Ala Ser Ser Pro

5 10 15

cct ccg aaa acc gag gca gcg agc gac ccc cag cat ccc gcg gcc tcc 154
 Pro Pro Lys Thr Glu Ala Ala Ser Asp Pro Gln His Pro Ala Ala Ser

20 25 30 35

gaa ggg gcc gcc gcc gcc gcc gcc tcg ccg cca ctg ctg cgc tgc cta 202
 Glu Gly Ala Ala Ala Ala Ala Ala Ser Pro Pro Leu Leu Arg Cys Leu

40 45 50

gtg ctc acc ggc ttt gga ggc tac gac aag gtg aag ctg cag agc cgg 250
 Val Leu Thr Gly Phe Gly Gly Tyr Asp Lys Val Lys Leu Gln Ser Arg

55 60 65

ccg gca gcg ccc ccg gcc cct ggg ccc ggc cag ctg acg ctg cgt ctg 298
 Pro Ala Ala Pro Pro Ala Pro Gly Pro Gly Gln Leu Thr Leu Arg Leu

70 75 80

cgg gcc tgc ggg ctc aac ttc gca gac ctc atg gct agg cag ggg ctg 346
 Arg Ala Cys Gly Leu Asn Phe Ala Asp Leu Met Ala Arg Gln Gly Leu

85 90 95

tac gac cgt ctc ccg cct ctg cct gtc act ccg ggc atg gag ggc gcg 394
 Tyr Asp Arg Leu Pro Pro Leu Pro Val Thr Pro Gly Met Glu Gly Ala

100 105 110 115

ggt gtt gtg atc gca gtg ggc gag gga gtc agc gac cgc aag gca gga 442

Gly Val Val Ile Ala Val Gly Glu Gly Val Ser Asp Arg Lys Ala Gly

120

125

130

gac cgg gtg atg gtg ttg aac cgg tca ggg atg tgg cag gaa gag gtg 490

Asp Arg Val Met Val Leu Asn Arg Ser Gly Met Trp Gln Glu Glu Val

135

140

145

act gtg ccc tcg gtc cag acc ttc ctg att cct gag gcc atg acc ttt 538

Thr Val Pro Ser Val Gln Thr Phe Leu Ile Pro Glu Ala Met Thr Phe

150

155

160

gag gaa gct gct gcc ttg ctc gtc aat tac att aca gcc tac atg gtc 586

Glu Glu Ala Ala Ala Leu Leu Val Asn Tyr Ile Thr Ala Tyr Met Val

165

170

175

ctc ttt gac ttc ggc aac cta cag cct ggc cac agc gtc ttg gta cac 634

Leu Phe Asp Phe Gly Asn Leu Gln Pro Gly His Ser Val Leu Val His

180

185

190

195

atg gct gca ggg ggt gtg ggt atg gct gcc gtg cag ctg tgc cgt aca 682

Met Ala Ala Gly Gly Val Gly Met Ala Ala Val Gln Leu Cys Arg Thr

200

205

210

gtg gag aat gtg aca gtg ttc gga acg gcc tcg gcc agc aag cac gag 730

Val Glu Asn Val Thr Val Phe Gly Thr Ala Ser Ala Ser Lys His Glu

215

220

225

gca ctg aag gag aat ggg gtc aca cat ccc atc gac tat cac acg act 778

124/735

Ala Leu Lys Glu Asn Gly Val Thr His Pro Ile Asp Tyr His Thr Thr

230

235

240

gac tac gtg gat gag atc aag aag att tcc cct aaa gga gtg gac att 826

Asp Tyr Val Asp Glu Ile Lys Lys Ile Ser Pro Lys Gly Val Asp Ile

245

250

255

gtc atg gac cct ctg ggt ggg tca gat act gcc aag ggc tac aac ctc 874

Val Met Asp Pro Leu Gly Gly Ser Asp Thr Ala Lys Gly Tyr Asn Leu

260

265

270

275

ctg aaa ccc atg ggc aaa gtc gtc acc tat gga atg gcc aac ctg ctg 922

Leu Lys Pro Met Gly Lys Val Val Thr Tyr Gly Met Ala Asn Leu Leu

280

285

290

acg ggc ccc aaa cgg aac ctg atg gcc ctg gcc cgg aca tgg tgg aat 970

Thr Gly Pro Lys Arg Asn Leu Met Ala Leu Ala Arg Thr Trp Trp Asn

295

300

305

cag ttc agc gtg aca gct ctg cag ctg ctg cag gcc aac cgg gct gtg 1018

Gln Phe Ser Val Thr Ala Leu Gln Leu Leu Gln Ala Asn Arg Ala Val

310

315

320

tgt ggc ttc cac ctg ggc tac ctg gat ggt gag gtg gag ctg gtc agt 1066

Cys Gly Phe His Leu Gly Tyr Leu Asp Gly Glu Val Glu Leu Val Ser

325

330

335

ggt gtg gtg gcc cgc ctc ctg gct ctg tac aac cag ggc cac atc aag 1114

Gly Val Val Ala Arg Leu Leu Ala Leu Tyr Asn Gln Gly His Ile Lys

340	345	350	355	
ccc cac att gac tca gtc tgg ccc ttc gag aag gtg gct gat gcc atg				1162
Pro His Ile Asp Ser Val Trp Pro Phe Glu Lys Val Ala Asp Ala Met				
	360	365	370	
aaa cag atg cag gag aag aag aat gtg ggc aag gtc ctc ctg gtt cca				1210
Lys Gln Met Gln Glu Lys Lys Asn Val Gly Lys Val Leu Leu Val Pro				
	375	380	385	
ggg cca gag aag gag aac tagggcaagt ggctgtgaga ccctagagac				1258
Gly Pro Glu Lys Glu Asn				
	390			
cagcgaaggg agaagttggg aagctacgtt ctgttggcca ccagacttgc atttcagcct				1318
ctgtcataat gctctgcctt cctcccccg aagttctctg tggatgatgac cgtctctccc				1378
tgccccctcc cgttctctga cctctgaaga ggttgggaag tgaccatttg gatgtctggg				1438
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ttgaaacgtc agctcaggat atggggccaa tctctgtgag tccagcatgt acctgtctct				1678
ccctagtgtc ccttcagcct gggtgacca gtgccgcct ctgggcttga ccagttccca				1738

atctcgctct ctgtcccaaa cttcttaage acaattgggc ttcttccatc tccaggtttt 1798

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cctcatcgtg gtctgtgcca tgtcccgtct ctatggtggt tgaggagaaa ggcggggaag 1918

cttctcage cttgcagata tgtgtggcat ttactagcca gagctctgaa aggcagtgc 1978

gtctgtttct tgtactggga ccaaagtaaa aatccaagca cattccccct gcagttaggg 2038

gaggccctac tgccttctca aagcagagag gcagcttate aaactcagcc caaaactctg 2098

tttcatggg tggggagatg gagcaggga gtacagagtg ggatggtcag gacctgggcc 2158

attgcaacca aatggggac ttcttgggta gggaggtcac tccctctact cactgagcta 2218

ggattaggga gggttattgc cccaaccatt gcaatgggag gtggaggga aggctcagcc 2278

tcctcattgt ctaaagagg cctaaatgtg tgaagtgcga tttctgcttt tgtgtacccc 2338

accaccccat taccacagct gcctttgtgt gtttgtgtca ataaaaagcc aaaccctg 2396

<210> 45

<211> 393

<212> PRT

<213> Homo sapiens

<400> 45

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1 5 10 15

Ser Ser Pro Pro Pro Lys Thr Glu Ala Ala Ser Asp Pro Gln His Pro

20 25 30

Ala Ala Ser Glu Gly Ala Ala Ala Ala Ala Ser Pro Pro Leu Leu

35 40 45

Arg Cys Leu Val Leu Thr Gly Phe Gly Gly Tyr Asp Lys Val Lys Leu

50 55 60

Gln Ser Arg Pro Ala Ala Pro Pro Ala Pro Gly Pro Gly Gln Leu Thr

65 70 75 80

Leu Arg Leu Arg Ala Cys Gly Leu Asn Phe Ala Asp Leu Met Ala Arg

85 90 95

Gln Gly Leu Tyr Asp Arg Leu Pro Pro Leu Pro Val Thr Pro Gly Met

100 105 110

Glu Gly Ala Gly Val Val Ile Ala Val Gly Glu Gly Val Ser Asp Arg

115 120 125

Lys Ala Gly Asp Arg Val Met Val Leu Asn Arg Ser Gly Met Trp Gln

130 135 140

Glu Glu Val Thr Val Pro Ser Val Gln Thr Phe Leu Ile Pro Glu Ala

128/735

agctgtgcac tctccatcca gctgtgcgct ctcgtcgga gtcccagcc atg tcc gac 58

Met Ser Asp

1

gag aga gag gta gcc gag gca gcg acc ggg gaa gac gcc tct tcg ccg 106

Glu Arg Glu Val Ala Glu Ala Ala Thr Gly Glu Asp Ala Ser Ser Pro

5

10

15

cct ccg aaa acc gag gca gcg agc gac ccc cag cat ccc gcg gcc tcc 154

Pro Pro Lys Thr Glu Ala Ala Ser Asp Pro Gln His Pro Ala Ala Ser

20

25

30

35

gaa ggg gcc gcc gcc gcc gcc gcc tcg ccg cca ctg ctg cgc tgc cta 202

Glu Gly Ala Ala Ala Ala Ala Ser Pro Pro Leu Leu Arg Cys Leu

40

45

50

gtg ctc acc ggc ttt gga ggc tac gac aag gtg aag ctg cag agc cgg 250

Val Leu Thr Gly Phe Gly Gly Tyr Asp Lys Val Lys Leu Gln Ser Arg

55

60

65

ccg gca gcg ccc ccg gcc cct ggg ccc ggc cag ctg acg ctg cgt ctg 298

Pro Ala Ala Pro Pro Ala Pro Gly Pro Gly Gln Leu Thr Leu Arg Leu

70

75

80

cgg gcc tgc ggg ctc aac ttc gca gac ctc atg gct agg cag ggg ctg 346

Arg Ala Cys Gly Leu Asn Phe Ala Asp Leu Met Ala Arg Gln Gly Leu

85

90

95

tac gac cgt ctc ccg cct ctg cct gtc act ccg ggc atg gag ggc gcg 394

Tyr Asp Arg Leu Pro Pro Leu Pro Val Thr Pro Gly Met Glu Gly Ala

100 105 110 115

ggt gtt gtg atc gca gtg ggc gag gga gtc agc gac cgc aag gca gga 442

Gly Val Val Ile Ala Val Gly Glu Gly Val Ser Asp Arg Lys Ala Gly

120 125 130

gac cgg gtg atg gtg ttg aac cgg tca ggg atg tgg cag gaa gag gtg 490

Asp Arg Val Met Val Leu Asn Arg Ser Gly Met Trp Gln Glu Glu Val

135 140 145

act gtg ccc tcg gtc cag acc ttc ctg att cct gag gcc atg acc ttt 538

Thr Val Pro Ser Val Gln Thr Phe Leu Ile Pro Glu Ala Met Thr Phe

150 155 160

gag gaa gct gct gcc ttg ctc gtc aat tac att aca gcc tac atg gtc 586

Glu Glu Ala Ala Ala Leu Leu Val Asn Tyr Ile Thr Ala Tyr Met Val

165 170 175

ctc ttt gac ttc ggc aac cta cag cct ggc cac agc gtc ttg gta cac 634

Leu Phe Asp Phe Gly Asn Leu Gln Pro Gly His Ser Val Leu Val His

180 185 190 195

atg gct gca ggg ggt gtg ggt atg gct gcc gtg cag ctg tgc cgt aca 682

Met Ala Ala Gly Gly Val Gly Met Ala Ala Val Gln Leu Cys Arg Thr

200 205 210

gtg gag aat gtg aca gtg ttc gga acg gcc tcg gcc agc aag cac gag 730

Val Glu Asn Val Thr Val Phe Gly Thr Ala Ser Ala Ser Lys His Glu

215

220

225

gca ctg aag gag aat ggg gtc aca cat ccc atc gac tat cac acg act 778
Ala Leu Lys Glu Asn Gly Val Thr His Pro Ile Asp Tyr His Thr Thr

230

235

240

gac tac gtg gat gag atc aag aag att tcc cct aaa gga gtg gac att 826
Asp Tyr Val Asp Glu Ile Lys Lys Ile Ser Pro Lys Gly Val Asp Ile

245

250

255

gtc atg gac cct ctg ggt ggg tca gat act gcc aag ggc tac aac ctc 874
Val Met Asp Pro Leu Gly Gly Ser Asp Thr Ala Lys Gly Tyr Asn Leu

260

265

270

275

ctg aaa ccc atg ggc aaa gtc gtc acc tat gga atg gcc aac ctg ctg 922
Leu Lys Pro Met Gly Lys Val Val Thr Tyr Gly Met Ala Asn Leu Leu

280

285

290

acg ggc ccc aaa cgg aac ctg atg gcc ctg gcc cgg aca tgg tgg aat 970
Thr Gly Pro Lys Arg Asn Leu Met Ala Leu Ala Arg Thr Trp Trp Asn

295

300

305

cag ttc agc gtg aca gct ctg cag ctg ctg cag gcc aac cgg gct gtg 1018
Gln Phe Ser Val Thr Ala Leu Gln Leu Leu Gln Ala Asn Arg Ala Val

310

315

320

tgt ggc ttc cac ctg ggc tac ctg gat ggt gag gtg gag ctg gtc agt 1066
Cys Gly Phe His Leu Gly Tyr Leu Asp Gly Glu Val Glu Leu Val Ser

325

330

335

ggt gtg gtg gcc cgc ctc ctg gct ctg tac aac cag ggc cac atc aag 1114
 Gly Val Val Ala Arg Leu Leu Ala Leu Tyr Asn Gln Gly His Ile Lys
 340 345 350 355

ccc cac att gac tca gtc tgg ccc ttc gag aag gtg gct gat gcc atg 1162
 Pro His Ile Asp Ser Val Trp Pro Phe Glu Lys Val Ala Asp Ala Met
 360 365 370

aaa cag atg cag gag aag aag aat gtg ggc aag gtc ctc ctg gtt cca 1210
 Lys Gln Met Gln Glu Lys Lys Asn Val Gly Lys Val Leu Leu Val Pro
 375 380 385

ggg cca gag aag cag aac tagggcaagt ggctgtgaga ccctagagac 1258
 Gly Pro Glu Lys Gln Asn
 390

cagcgaaggg agaagttggg aagctacgtt ctgttgcca ccagacttgc atttcagcct 1318

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tcctcattgt ctaaatgagg cctaaatgtg tgaagtgcga tttctgcttt tgtgtacccc 2338

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<211> 138

<212> PRT

<213> Homo sapiens

<400> 47

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Phe Gly Val Phe Phe Leu Phe Phe Gly Met Ile Leu Phe Phe Asp Lys

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Ala Leu Leu Ala Ile Gly Asn Val Leu Phe Val Ala Gly Leu Ala Phe

35 40 45

Val Ile Gly Leu Glu Arg Thr Phe Arg Phe Phe Phe Gln Lys His Lys

50 55 60

Met Lys Ala Thr Gly Phe Phe Leu Gly Gly Val Phe Val Val Leu Ile

65 70 75 80

Gly Trp Pro Leu Ile Gly Met Ile Phe Glu Ile Tyr Gly Phe Phe Leu

85 90 95

Leu Phe Arg Gly Phe Phe Pro Val Val Val Gly Phe Ile Arg Arg Val

100 105 110

Pro Val Leu Gly Ser Leu Leu Asn Leu Pro Gly Ile Arg Ser Phe Val

115 120 125

Asp Lys Val Gly Glu Ser Asn Asn Met Val

136/735

40

45

50

tta gaa aga aca ttc aga ttc ttc ttc caa aaa cat aaa atg aaa gct 310
Leu Glu Arg Thr Phe Arg Phe Phe Phe Gln Lys His Lys Met Lys Ala

55

60

65

aca ggt ttt ttt ctg ggt ggt gta ttt gta gtc ctt att ggt tgg cct 358
Thr Gly Phe Phe Leu Gly Gly Val Phe Val Val Leu Ile Gly Trp Pro

70

75

80

ttg ata ggc atg atc ttc gaa att tat gga ttt ttt ctc ttg ttc agg 406
Leu Ile Gly Met Ile Phe Glu Ile Tyr Gly Phe Phe Leu Leu Phe Arg

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ggc ttc ttt cct gtc gtt gtt ggc ttt att aga aga gtg cca gtc ctt 454
Gly Phe Phe Pro Val Val Val Gly Phe Ile Arg Arg Val Pro Val Leu

100

105

110

115

gga tcc ctc cta aat tta cct gga att aga tca ttt gta gat aaa gtt 502
Gly Ser Leu Leu Asn Leu Pro Gly Ile Arg Ser Phe Val Asp Lys Val

120

125

130

gga gaa agc aac aat atg gta taacaacaag tgaatttgaa gactcattta 553
Gly Glu Ser Asn Asn Met Val

135

aaatattgtg ttatttataa agtcatttga agaattattca gcacaaaatt aaattacatg 613

aaatagcttg taatgttctt tacaggagtt taaaacgtat agcctacaaa gtaccagcag 673

caaattagca aagaagcagt gaaaacaggc ttctactcaa gtgaactaag aagaagtcag 733

caagcaaact gagagagggtg aaatccatgt taatgatgct taagaaactc ttgaaggcta 793

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gtctcattga atagtattat tgaagatact aaatgatgca aaccaaatgg attttttcca 1393

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taaaaggtta aacttatggc tgttttttaa gggctattca tttaatctga gttttccctt 1573

attttcagct ttttctage atataatagt cattaagcat gacatatect tcatatgate 1633

actcatcttg agttaattag aaaatacctg agttcacgtg ctaaagtcac ttcactgtaa 1693

taaactgact atggtttctt aagaacatga cactaaaaaa aaagtgggtt ttttccaccg 1753

ttgctgatta ttagacagta ggaaatagct gttttcttta gttttacaag atgtgacagc 1813

tttagtggtg gatgtaggga aacatttcaa cagccatagt actatttggt ttaccactga 1873

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aatctgtggt atttatttac aaacatgtct acaaaaatag attacagctt attttatttt 1993

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cacttgga ga gtgtcaaata catactttga ggattgactt tatataaggt gccctgtaga 2293

actctgttac acatattttt gacctatatt atttacaatg tcttgataat tetacctttt 2353

tagagcaaga atagtatctg ctaatgtaag ggacatctgt atttaactcc tttgtagaca 2413

tgaatttcta tcaaaatggt ctttgactg taacagagat tcttttttc aataatctta 2473

attcaaaagc attattagac ttgaaagggt ttgataatct cccagtcctt agtaaagatt 2533

gagagaggct ggagcagttt tcagttttta atgagtcctg agttaatatc aaatgtgagt 2593

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cagccttctg tctgtaacaa aaatgtactt tatagagatg gaggaaaagg tctaatacta 2773

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gaatgttttt cttttccct tataaattgt aattcctgaa atactgctgc tttaaaaagt 2893

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<211> 359

<212> PRT

<213> Homo sapiens

<400> 49

Met Ser Lys Glu Thr Ile Ile Lys Cys Glu Lys Gln Lys Pro Arg Phe

Ser Pro His Gly Gln Thr Arg Pro Pro Ala Ser Leu Lys His Ile His

165

170

175

Leu Met Pro Leu Ser Gln Ile Lys Lys Val Leu Asp Ile Arg Glu Thr

180

185

190

Glu Asp Cys His Asn Ala Phe Ala Leu Leu Val Arg Pro Pro Thr Glu

195

200

205

Gln Ala Asn Val Leu Leu Ser Phe Gln Met Thr Ser Asp Glu Leu Pro

210

215

220

Lys Glu Asn Trp Leu Lys Met Leu Cys Arg His Val Ala Asn Thr Ile

225

230

235

240

Cys Lys Ala Asp Ala Glu Asn Leu Ile Tyr Thr Ala Asp Pro Glu Ser

245

250

255

Phe Glu Val Asn Thr Lys Asp Met Asp Ser Thr Leu Ser Arg Ala Ser

260

265

270

Arg Ala Ile Lys Lys Thr Ser Lys Lys Val Thr Arg Ala Phe Ser Phe

275

280

285

Ser Lys Thr Pro Lys Arg Ala Leu Arg Arg Ala Leu Met Thr Ser His

290

295

300

Gly Ser Val Glu Gly Arg Ser Pro Ser Ser Asn Asp Lys His Val Met

305

310

315

320

atgagagcaa aagcattggt gacatttttc tgaaatattc aaaagatttg gtaaaaacct 300

accctccctt tgtaaacttc ttigaa atg agc aag gaa aca att att aaa tgt 353

Met Ser Lys Glu Thr Ile Ile Lys Cys

1

5

gaa aaa cag aaa cca aga ttt cat gct ttt ctc aag ata aac caa gca 401

Glu Lys Gln Lys Pro Arg Phe His Ala Phe Leu Lys Ile Asn Gln Ala

10

15

20

25

aaa cca gaa tgt gga cgg cag agc ctt gtt gaa ctt ctt atc cga cca 449

Lys Pro Glu Cys Gly Arg Gln Ser Leu Val Glu Leu Leu Ile Arg Pro

30

35

40

gta cag agg tta ccc agt gtt gca tta ctt tta aat gat ctt aag aag 497

Val Gln Arg Leu Pro Ser Val Ala Leu Leu Leu Asn Asp Leu Lys Lys

45

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55

cat aca gct gat gaa aat cca gac aaa agc act tta gaa aaa gct att 545

His Thr Ala Asp Glu Asn Pro Asp Lys Ser Thr Leu Glu Lys Ala Ile

60

65

70

gga tca ctg aag gaa gta atg acg cat att aat gag gat aag aga aaa 593

Gly Ser Leu Lys Glu Val Met Thr His Ile Asn Glu Asp Lys Arg Lys

75

80

85

aca gaa gct caa aag caa att ttt gat gtt gtt tat gaa gta gat gga 641

Thr Glu Ala Gln Lys Gln Ile Phe Asp Val Val Tyr Glu Val Asp Gly

90

95

100

105

tgc cca gct aat ctt tta tct tct cac cga agc tta gta cag cgg gtt 689

Cys Pro Ala Asn Leu Leu Ser Ser His Arg Ser Leu Val Gln Arg Val

110

115

120

gaa aca att tct cta ggt gag cac ccc tgt gac aga gga gaa caa gta 737

Glu Thr Ile Ser Leu Gly Glu His Pro Cys Asp Arg Gly Glu Gln Val

125

130

135

act ctc ttc ctc ttc aat gat tgc cta gag ata gca aga aaa cgg cac 785

Thr Leu Phe Leu Phe Asn Asp Cys Leu Glu Ile Ala Arg Lys Arg His

140

145

150

aag gtt att ggc act ttt agg agt cct cat ggc caa acc cga ccc cca 833

Lys Val Ile Gly Thr Phe Arg Ser Pro His Gly Gln Thr Arg Pro Pro

155

160

165

gct tct ctt aag cat att cac cta atg cct ctt tct cag att aag aag 881

Ala Ser Leu Lys His Ile His Leu Met Pro Leu Ser Gln Ile Lys Lys

170

175

180

185

gta ttg gac ata aga gag aca gaa gat tgc cat aat gct ttt gcc ttg 929

Val Leu Asp Ile Arg Glu Thr Glu Asp Cys His Asn Ala Phe Ala Leu

190

195

200

ctt gtg agg cca cca aca gag cag gca aat gtg cta ctc agt ttc cag 977

Leu Val Arg Pro Pro Thr Glu Gln Ala Asn Val Leu Leu Ser Phe Gln

205

210

215

Met Thr Ser Asp Glu Leu Pro Lys Glu Asn Trp Leu Lys Met Leu Cys
220 225 230

cga cat gta gct aac acc att tgt aaa gca gat gct gag aat ctt att 1073
Arg His Val Ala Asn Thr Ile Cys Lys Ala Asp Ala Glu Asn Leu Ile
235 240 245

tat act gct gat cca gaa tcc ttt gaa gta aat aca aaa gat atg gac 1121
Tyr Thr Ala Asp Pro Glu Ser Phe Glu Val Asn Thr Lys Asp Met Asp
250 255 260 265

agt aca ttg agt aga gca tca aga gca ata aaa aag act tca aaa aag 1169
Ser Thr Leu Ser Arg Ala Ser Arg Ala Ile Lys Lys Thr Ser Lys Lys
270 275 280

gtt aca aga gca ttc tct ttc tcc aaa act cca aaa aga gct ctt cga 1217
Val Thr Arg Ala Phe Ser Phe Ser Lys Thr Pro Lys Arg Ala Leu Arg
285 290 295

agg gct ctt atg aca tcc cac ggc tca gtg gag gga aga agt cct tcc 1265
Arg Ala Leu Met Thr Ser His Gly Ser Val Glu Gly Arg Ser Pro Ser
300 305 310

agc aat gat aag cat gta atg agt cgt ctt tct agc aca tca tca tta 1313
Ser Asn Asp Lys His Val Met Ser Arg Leu Ser Ser Thr Ser Ser Leu
315 320 325

gca ggt atc cct tct ccc tcc ctt gtc agc ctt cct tcc ttc ttt gaa 1361
147/735

Ala Gly Ile Pro Ser Pro Ser Leu Val Ser Leu Pro Ser Phe Phe Glu

330

335

340

345

agg aga agt cat acg tta agt aga tct aca act cat ttg ata

1403

Arg Arg Ser His Thr Leu Ser Arg Ser Thr Thr His Leu Ile

350

355

tgaagcgтта ccaaaatctt aaattataga aatgtataga cacctcatac tcaaataaga 1463

aactgactta aatggtactt gtaattagca cttggtgaaa gctggaagga agataaataa 1523

cactaaacta tgctatttga tttttcttct tgaaagagta aggtttacct gttacatttt 1583

caagttaatt catgtaaaaa atgatatgta ttttgatgta atttatctct tgtttgaatc 1643

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aatgacatca taatactgga tgaaaacttg catagaattc tgattaaata gtgggtctgt 1883

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agtaagaact ttgtaaataa atacctaaaa ccc 2636

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<211> 883

<212> PRT

<213> Homo sapiens

<400> 51

Met Ala Glu Asn Ser Val Leu Thr Ser Thr Thr Gly Arg Thr Ser Leu

1

5

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15

Ala Asp Ser Ser Ile Phe Asp Ser Lys Val Thr Glu Ile Ser Lys Glu

20

25

30

Asn Leu Leu Ile Gly Ser Thr Ser Tyr Val Glu Glu Glu Met Pro Gln

35

40

45

Ile Glu Thr Arg Val Ile Leu Val Gln Glu Ala Gly Lys Gln Glu Glu

50

55

60

Leu Thr Lys Ala Leu Lys Asp Ile Lys Val Gly Phe Val Lys Met Glu

65

70

75

80

Ser Val Glu Glu Phe Glu Gly Leu Asp Ser Pro Glu Phe Glu Asn Val

85

90

95

Phe Val Val Thr Asp Phe Gln Asp Ser Val Phe Asn Asp Leu Tyr Lys

100

105

110

Ala Asp Cys Arg Val Ile Gly Pro Pro Val Val Leu Asn Cys Ser Gln

115

120

125

Lys Gly Glu Pro Leu Pro Phe Ser Cys Arg Pro Leu Tyr Cys Thr Ser

130

135

140

Met Met Asn Leu Val Leu Cys Phe Thr Gly Phe Arg Lys Lys Glu Glu

145

150

155

160

Leu Val Arg Leu Val Thr Leu Val His His Met Gly Gly Val Ile Arg

150/735

.. .. .

165

170

175

Lys Asp Phe Asn Ser Lys Val Thr His Leu Val Ala Asn Cys Thr Gln

180

185

190

Gly Glu Lys Phe Arg Val Ala Val Ser Leu Gly Thr Pro Ile Met Lys

195

200

205

Pro Glu Trp Ile Tyr Lys Ala Trp Glu Arg Arg Asn Glu Gln Asp Phe

210

215

220

Tyr Ala Ala Val Asp Asp Phe Arg Asn Glu Phe Lys Val Pro Pro Phe

225

230

235

240

Gln Asp Cys Ile Phe Ser Phe Leu Gly Phe Ser Asp Glu Glu Lys Thr

245

250

255

Asn Met Glu Glu Met Thr Glu Met Gln Gly Gly Lys Tyr Leu Pro Leu

260

265

270

Gly Asp Glu Arg Cys Thr His Leu Val Val Glu Glu Asn Ile Val Lys

275

280

285

Asp Leu Pro Phe Glu Pro Ser Lys Lys Leu Tyr Val Val Lys Gln Glu

290

295

300

Trp Phe Trp Gly Ser Ile Gln Met Asp Ala Arg Ala Gly Glu Thr Met

305

310

315

320

Tyr Leu Tyr Glu Lys Ala Asn Thr Pro Glu Leu Lys Lys Ser Val Ser

325

330

335

Met Leu Ser Leu Asn Thr Pro Asn Ser Asn Arg Lys Arg Arg Arg Leu

340

345

350

Lys Glu Thr Leu Ala Gln Leu Ser Arg Asp Thr Asp Val Ser Pro Phe

355

360

365

Pro Pro Arg Lys Arg Pro Ser Ala Glu His Ser Leu Ser Ile Gly Ser

370

375

380

Leu Leu Asp Ile Ser Asn Thr Pro Glu Ser Ser Ile Asn Tyr Gly Asp

385

390

395

400

Thr Pro Lys Ser Cys Thr Lys Ser Ser Lys Ser Ser Thr Pro Val Pro

405

410

415

Ser Lys Gln Ser Ala Arg Trp Gln Val Ala Lys Glu Leu Tyr Gln Thr

420

425

430

Glu Ser Asn Tyr Val Asn Ile Leu Ala Thr Ile Ile Gln Leu Phe Gln

435

440

445

Val Pro Leu Glu Glu Glu Gly Gln Arg Gly Gly Pro Ile Leu Ala Pro

450

455

460

Glu Glu Ile Lys Thr Ile Phe Gly Ser Ile Pro Asp Ile Phe Asp Val

465

470

475

480

His Thr Lys Ile Lys Asp Asp Leu Glu Asp Leu Ile Val Asn Trp Asp
485 490 495

Glu Ser Lys Ser Ile Gly Asp Ile Phe Leu Lys Tyr Ser Lys Asp Leu
500 505 510

Val Lys Thr Tyr Pro Pro Phe Val Asn Phe Phe Glu Met Ser Lys Glu
515 520 525

Thr Ile Ile Lys Cys Glu Lys Gln Lys Pro Arg Phe His Ala Phe Leu
530 535 540

Lys Ile Asn Gln Ala Lys Pro Glu Cys Gly Arg Gln Ser Leu Val Glu
545 550 555 560

Leu Leu Ile Arg Pro Val Gln Arg Leu Pro Ser Val Ala Leu Leu Leu
565 570 575

Asn Asp Leu Lys Lys His Thr Ala Asp Glu Asn Pro Asp Lys Ser Thr
580 585 590

Leu Glu Lys Ala Ile Gly Ser Leu Lys Glu Val Met Thr His Ile Asn
595 600 605

Glu Asp Lys Arg Lys Thr Glu Ala Gln Lys Gln Ile Phe Asp Val Val
610 615 620

Tyr Glu Val Asp Gly Cys Pro Ala Asn Leu Leu Ser Ser His Arg Ser
153/735

625 630 635 640

Leu Val Gln Arg Val Glu Thr Ile Ser Leu Gly Glu His Pro Cys Asp
 645 650 655

Arg Gly Glu Gln Val Thr Leu Phe Leu Phe Asn Asp Cys Leu Glu Ile
 660 665 670

Ala Arg Lys Arg His Lys Val Ile Gly Thr Phe Arg Ser Pro His Gly
 675 680 685

Gln Thr Arg Pro Pro Ala Ser Leu Lys His Ile His Leu Met Pro Leu
 690 695 700

Ser Gln Ile Lys Lys Val Leu Asp Ile Arg Glu Thr Glu Asp Cys His
 705 710 715 720

Asn Ala Phe Ala Leu Leu Val Arg Pro Pro Thr Glu Gln Ala Asn Val
 725 730 735

Leu Leu Ser Phe Gln Met Thr Ser Asp Glu Leu Pro Lys Glu Asn Trp
 740 745 750

Leu Lys Met Leu Cys Arg His Val Ala Asn Thr Ile Cys Lys Ala Asp
 755 760 765

Ala Glu Asn Leu Ile Tyr Thr Ala Asp Pro Glu Ser Phe Glu Val Asn
 770 775 780

<222> (29).. (2677)

<400> 52

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Met Ala Glu Asn Ser Val Leu Thr

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Ser Thr Thr Gly Arg Thr Ser Leu Ala Asp Ser Ser Ile Phe Asp Ser

10

15

20

aaa gtt act gag att tcc aag gaa aac tta ctt att gga tct act tca 148

Lys Val Thr Glu Ile Ser Lys Glu Asn Leu Leu Ile Gly Ser Thr Ser

25

30

35

40

tat gta gaa gaa gag atg cct cag att gaa aca aga gtg ata ttg gtt 196

Tyr Val Glu Glu Glu Met Pro Gln Ile Glu Thr Arg Val Ile Leu Val

45

50

55

caa gaa gct gga aaa caa gaa gaa ctt aca aaa gcc tta aag gac att 244

Gln Glu Ala Gly Lys Gln Glu Glu Leu Thr Lys Ala Leu Lys Asp Ile

60

65

70

aaa gtg ggc ttt gta aag atg gag tca gtg gaa gaa ttt gaa ggt ttg 292

Lys Val Gly Phe Val Lys Met Glu Ser Val Glu Glu Phe Glu Gly Leu

75

80

85

gat tct ccg gaa ttt gaa aat gta ttt gta gtc acg gac ttt cag gat 340

Asp Ser Pro Glu Phe Glu Asn Val Phe Val Val Thr Asp Phe Gln Asp

156/735

90

95

100

tct gtc ttt aat gac ctc tac aag gct gat tgt aga gtt att gga cca 388

Ser Val Phe Asn Asp Leu Tyr Lys Ala Asp Cys Arg Val Ile Gly Pro

105

110

115

120

cca gtt gta tta aat tgt tca caa aaa gga gag cct ttg cca ttt tca 436

Pro Val Val Leu Asn Cys Ser Gln Lys Gly Glu Pro Leu Pro Phe Ser

125

130

135

tgt cgc ccg ttg tat tgt aca agt atg atg aat cta gta cta tgc ttt 484

Cys Arg Pro Leu Tyr Cys Thr Ser Met Met Asn Leu Val Leu Cys Phe

140

145

150

act gga ttt agg aaa aaa gaa gaa cta gtc agg ttg gtg aca ttg gtc 532

Thr Gly Phe Arg Lys Lys Glu Glu Leu Val Arg Leu Val Thr Leu Val

155

160

165

cat cac atg ggt gga gtt att cga aaa gac ttt aat tca aaa gtt aca 580

His His Met Gly Gly Val Ile Arg Lys Asp Phe Asn Ser Lys Val Thr

170

175

180

cat ttg gtg gca aat tgt aca caa gga gaa aaa ttc agg gtt gct gtg 628

His Leu Val Ala Asn Cys Thr Gln Gly Glu Lys Phe Arg Val Ala Val

185

190

195

200

agt cta ggt act cca att atg aag cca gaa tgg att tat aaa gct tgg 676

Ser Leu Gly Thr Pro Ile Met Lys Pro Glu Trp Ile Tyr Lys Ala Trp

205

210

215

gaa agg cgg aat gaa cag gat ttc tat gca gca gtt gat gac ttt aga 724

Glu Arg Arg Asn Glu Gln Asp Phe Tyr Ala Ala Val Asp Asp Phe Arg

220

225

230

aat gaa ttt aaa gtt cct cca ttt caa gat tgt att ttt agt ttc ctg 772

Asn Glu Phe Lys Val Pro Pro Phe Gln Asp Cys Ile Phe Ser Phe Leu

235

240

245

gga ttt tca gat gaa gag aaa acc aat atg gaa gaa atg act gaa atg 820

Gly Phe Ser Asp Glu Glu Lys Thr Asn Met Glu Glu Met Thr Glu Met

250

255

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caa gga ggt aaa tat tta ccg ctt gga gat gaa aga tgc act cac ctt 868

Gln Gly Gly Lys Tyr Leu Pro Leu Gly Asp Glu Arg Cys Thr His Leu

265

270

275

280

gta gtt gaa gag aat ata gta aaa gat ctt ccc ttt gaa cct tca aag 916

Val Val Glu Glu Asn Ile Val Lys Asp Leu Pro Phe Glu Pro Ser Lys

285

290

295

aaa ctt tat gtt gtc aag caa gag tgg ttc tgg gga agc att caa atg 964

Lys Leu Tyr Val Val Lys Gln Glu Trp Phe Trp Gly Ser Ile Gln Met

300

305

310

gat gcc cga gct gga gaa act atg tat tta tat gaa aag gca aat act 1012

Asp Ala Arg Ala Gly Glu Thr Met Tyr Leu Tyr Glu Lys Ala Asn Thr

315

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cct gag ctc aag aaa tca gtg tca atg ctt tct cta aat acc cct aac 1060

Pro Glu Leu Lys Lys Ser Val Ser Met Leu Ser Leu Asn Thr Pro Asn

330

335

340

agc aat cgc aaa cga cgt cgt tta aaa gaa aca ctt gct cag ctt tca 1108

Ser Asn Arg Lys Arg Arg Arg Leu Lys Glu Thr Leu Ala Gln Leu Ser

345

350

355

360

aga gat aca gac gtg tca cca ttt cca ccc cgt aag cgc cca tca gct 1156

Arg Asp Thr Asp Val Ser Pro Phe Pro Pro Arg Lys Arg Pro Ser Ala

365

370

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gag cat tcc ctt tcc ata ggg tca ctc cta gat atc tcc aac aca cca 1204

Glu His Ser Leu Ser Ile Gly Ser Leu Leu Asp Ile Ser Asn Thr Pro

380

385

390

gag tct agc att aac tat gga gac acc cca aag tct tgt act aag tct 1252

Glu Ser Ser Ile Asn Tyr Gly Asp Thr Pro Lys Ser Cys Thr Lys Ser

395

400

405

tct aaa agc tcc act cca gtt cct tca aag cag tca gca agg tgg caa 1300

Ser Lys Ser Ser Thr Pro Val Pro Ser Lys Gln Ser Ala Arg Trp Gln

410

415

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gtt gca aaa gag ctt tat caa act gaa agt aat tat gtt aat ata ttg 1348

Val Ala Lys Glu Leu Tyr Gln Thr Glu Ser Asn Tyr Val Asn Ile Leu

425

430

435

440

gca aca att att cag tta ttt caa gta cca ttg gaa gag gaa gga caa 1396

Ala Thr Ile Ile Gln Leu Phe Gln Val Pro Leu Glu Glu Glu Gly Gln

445

450

455

cgt ggt gga cct atc ctt gca cca gag gag att aag act att ttt ggt 1444

Arg Gly Gly Pro Ile Leu Ala Pro Glu Glu Ile Lys Thr Ile Phe Gly

460

465

470

agc atc cca gat atc ttt gat gta cac act aag ata aag gat gat ctt 1492

Ser Ile Pro Asp Ile Phe Asp Val His Thr Lys Ile Lys Asp Asp Leu

475

480

485

gaa gac ctt ata gtt aat tgg gat gag agc aaa agc att ggt gac att 1540

Glu Asp Leu Ile Val Asn Trp Asp Glu Ser Lys Ser Ile Gly Asp Ile

490

495

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ttt ctg aaa tat tca aaa gat ttg gta aaa acc tac cct ccc ttt gta 1588

Phe Leu Lys Tyr Ser Lys Asp Leu Val Lys Thr Tyr Pro Pro Phe Val

505

510

515

520

aac ttc ttt gaa atg agc aag gaa aca att att aaa tgt gaa aaa cag 1636

Asn Phe Phe Glu Met Ser Lys Glu Thr Ile Ile Lys Cys Glu Lys Gln

525

530

535

aaa cca aga ttt cat gct ttt ctc aag ata aac caa gca aaa cca gaa 1684

Lys Pro Arg Phe His Ala Phe Leu Lys Ile Asn Gln Ala Lys Pro Glu

540

545

550

tgt gga cgg cag agc ctt gtt gaa ctt ctt atc cga cca gta cag agg 1732

Cys Gly Arg Gln Ser Leu Val Glu Leu Leu Ile Arg Pro Val Gln Arg

160/735

555	560	565	
tta ccc agt gtt gca tta ctt tta aat gat ctt aag aag cat aca gct			1780
Leu Pro Ser Val Ala Leu Leu Leu Asn Asp Leu Lys Lys His Thr Ala			
570	575	580	
gat gaa aat cca gac aaa agc act tta gaa aaa gct att gga tca ctg			1828
Asp Glu Asn Pro Asp Lys Ser Thr Leu Glu Lys Ala Ile Gly Ser Leu			
585	590	595	600
aag gaa gta atg acg cat att aat gag gat aag aga aaa aca gaa gct			1876
Lys Glu Val Met Thr His Ile Asn Glu Asp Lys Arg Lys Thr Glu Ala			
	605	610	615
caa aag caa att ttt gat gtt gtt tat gaa gta gat gga tgc cca gct			1924
Gln Lys Gln Ile Phe Asp Val Val Tyr Glu Val Asp Gly Cys Pro Ala			
620	625	630	
aat ctt tta tct tct cac cga agc tta gta cag cgg gtt gaa aca att			1972
Asn Leu Leu Ser Ser His Arg Ser Leu Val Gln Arg Val Glu Thr Ile			
635	640	645	
tct cta ggt gag cac ccc tgt gac aga gga gaa caa gta act ctc ttc			2020
Ser Leu Gly Glu His Pro Cys Asp Arg Gly Glu Gln Val Thr Leu Phe			
650	655	660	
ctc ttc aat gat tgc cta gag ata gca aga aaa cgg cac aag gtt att			2068
Leu Phe Asn Asp Cys Leu Glu Ile Ala Arg Lys Arg His Lys Val Ile			
665	670	675	680

ggc act ttt agg agt cct cat ggc caa acc cga ccc cca gct tct ctt 2116
Gly Thr Phe Arg Ser Pro His Gly Gln Thr Arg Pro Pro Ala Ser Leu
685 690 695

aag cat att cac cta atg cct ctt tct cag att aag aag gta ttg gac 2164
Lys His Ile His Leu Met Pro Leu Ser Gln Ile Lys Lys Val Leu Asp
700 705 710

ata aga gag aca gaa gat tgc cat aat gct ttt gcc ttg ctt gtg agg 2212
Ile Arg Glu Thr Glu Asp Cys His Asn Ala Phe Ala Leu Leu Val Arg
715 720 725

cca cca aca gag cag gca aat gtg cta ctc agt ttc cag atg aca tca 2260
Pro Pro Thr Glu Gln Ala Asn Val Leu Leu Ser Phe Gln Met Thr Ser
730 735 740

gat gaa ctt cca aaa gaa aac tgg cta aag atg ctg tgt cga cat gta 2308
Asp Glu Leu Pro Lys Glu Asn Trp Leu Lys Met Leu Cys Arg His Val
745 750 755 760

gct aac acc att tgt aaa gca gat gct gag aat ctt att tat act gct 2356
Ala Asn Thr Ile Cys Lys Ala Asp Ala Glu Asn Leu Ile Tyr Thr Ala
765 770 775

gat cca gaa tcc ttt gaa gta aat aca aaa gat atg gac agt aca ttg 2404
Asp Pro Glu Ser Phe Glu Val Asn Thr Lys Asp Met Asp Ser Thr Leu
780 785 790

agt aga gca tca aga gca ata aaa aag act tca aaa aag gtt aca aga 2452

Ser Arg Ala Ser Arg Ala Ile Lys Lys Thr Ser Lys Lys Val Thr Arg

795

800

805

gca ttc tct ttc tcc aaa act cca aaa aga gct ctt cga agg gct ctt 2500

Ala Phe Ser Phe Ser Lys Thr Pro Lys Arg Ala Leu Arg Arg Ala Leu

810

815

820

atg aca tcc cac ggc tca gtg gag gga aga agt cct tcc agc aat gat 2548

Met Thr Ser His Gly Ser Val Glu Gly Arg Ser Pro Ser Ser Asn Asp

825

830

835

840

aag cat gta atg agt cgt ctt tct agc aca tca tca tta gca ggt atc 2596

Lys His Val Met Ser Arg Leu Ser Ser Thr Ser Ser Leu Ala Gly Ile

845

850

855

cct tct ccc tcc ctt gtc agc ctt cct tcc ttc ttt gaa agg aga agt 2644

Pro Ser Pro Ser Leu Val Ser Leu Pro Ser Phe Phe Glu Arg Arg Ser

860

865

870

cat acg tta agt aga tct aca act cat ttg ata tgaagcgta ccaaaatctt 2697

His Thr Leu Ser Arg Ser Thr Thr His Leu Ile

875

880

aaattataga aatgtataga cacctcatatc tcaaataaga aactgactta aatggtactt 2757

gtaattagca cttggtgaaa gctggaagga agataaataa cactaaacta tgctatttga 2817

ttttttctt tgaagagta aggtttacct gttacatttt caagttaatt catgtaaaaa 2877

atgatagtga ttttgatgta atttatctct tgtttgaatc tgtcattcaa aggccaataa 2937

tttaagttgc tatkagctga tattagtagc ttgcaacce tgatagagta aataaatttt 2997

atgggcgggt gccaaatact gctgtgaatc tatttgtata gtatccatga atgaatttat 3057

ggaaatagat atttgtgcag ctcaatttat gcagagatta aatgacatca taatactgga 3117

tgaaaacttg catagaattc tgattaaata gtgggtctgt ttcacatgtg cagtttgaag 3177

tatttaaata accactcctt tcacagtta ttttcttctc aagcgtttc aagatctagc 3237

atgtggattt taaaagattt gccctcatta acaagaataa catttaaagg agattgtttc 3297

aaaatatttt tgcaaattga gataaggaca gaaagattga gaaacattgt atattttgca 3357

aaaacaagat gttttagct gtttcagaga gactacggtg tatttatggt aattttatcc 3417

actagcaaat ctgatttag ttgatagtg tgtggaattt tattttgaag gataagacca 3477

tgggaaaatt gtggtaaaga ctgtttgtac ccttcattgaa ataattctga agttgccatc 3537

agttttacta atcttctgtg aaatgcatag atatgcgcat gttcaacttt ttattgtggt 3597

cttataatta aatgtaaaat tgaaaattca ttgctgttt caaagtgtga tatctttcac 3657

aatagccttt ttatagtcag taattcagaa taatcaagtt catatggata aatgcatttt 3717

tatttcctat ttcttttaggg agtgctacaa atgtttgtca cttaaatttc aagtttctgt 3777

tttaatagtt aactgactat agattgtttt ctatgccatg tatgtgccac ttctgagagt 3837

agtaaatgac tctttgctac attttaaaag caattgtatt agtaagaact ttgtaaataa 3897

atacctaataa ccc 3910

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- <211> 622
- <212> PRT
- <213> Homo sapiens

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Pro His Pro Pro Gly Phe Gly Arg Tyr Gly Ile Cys Ala His Glu Asn
20 25 30

Lys Glu Leu Ala Asn Ala Arg Glu Ala Leu Pro Leu Ile Glu Asp Ser
35 40 45

Ser Asn Cys Asp Ile Val Lys Ala Thr Gln Tyr Gly Ile Phe Glu Arg
50 55 60

Cys Lys Glu Leu Val Glu Ala Gly Tyr Asp Val Arg Gln Pro Asp Lys
65 70 75 80

Glu Asn Val Ser Leu Leu His Trp Ala Ala Ile Asn Asn Arg Leu Asp
85 90 95

Leu Val Lys Phe Tyr Ile Ser Lys Gly Ala Val Val Asp Gln Leu Gly
100 105 110

Gly Asp Leu Asn Ser Thr Pro Leu His Trp Ala Ile Arg Gln Gly His
115 120 125

Leu Pro Met Val Ile Leu Leu Leu Gln His Gly Ala Asp Pro Thr Leu
130 135 140

Ile Asp Gly Glu Gly Phe Ser Ser Ile His Leu Ala Val Leu Phe Gln
145 150 155 160

His Met Pro Ile Ile Ala Tyr Leu Ile Ser Lys Gly Gln Ser Val Asn
165 170 175

Met Thr Asp Val Asn Gly Gln Thr Pro Leu Met Leu Ser Ala His Lys
180 185 190

Val Ile Gly Pro Glu Pro Thr Gly Phe Leu Leu Lys Phe Asn Pro Ser
195 200 205

Leu Asn Val Val Asp Lys Ile His Gln Asn Thr Pro Leu His Trp Ala
210 215 220

Val Ala Ala Gly Asn Val Asn Ala Val Asp Lys Leu Leu Glu Ala Gly
166/735

225 230 235 240

Ser Ser Leu Asp Ile Gln Asn Val Lys Gly Glu Thr Pro Leu Asp Met

245 250 255

Ala Leu Gln Asn Lys Asn Gln Leu Ile Ile His Met Leu Lys Thr Glu

260 265 270

Ala Lys Met Arg Ala Asn Gln Lys Phe Arg Leu Trp Arg Trp Leu Gln

275 280 285

Lys Cys Glu Leu Phe Leu Leu Leu Met Leu Ser Val Ile Thr Met Trp

290 295 300

Ala Ile Gly Tyr Ile Leu Asp Phe Asn Ser Asp Ser Trp Leu Leu Lys

305 310 315 320

Gly Cys Leu Leu Val Thr Leu Phe Phe Leu Thr Ser Leu Phe Pro Arg

325 330 335

Phe Leu Val Gly Tyr Lys Asn Leu Val Tyr Leu Pro Thr Ala Phe Leu

340 345 350

Leu Ser Ser Val Phe Trp Ile Phe Met Thr Trp Phe Ile Leu Phe Phe

355 360 365

Pro Asp Leu Ala Gly Ala Pro Phe Tyr Phe Ser Phe Ile Phe Ser Ile

370 375 380

Val Ala Phe Leu Tyr Phe Phe Tyr Lys Thr Trp Ala Thr Asp Pro Gly
385 390 395 400

Phe Thr Lys Ala Ser Glu Glu Glu Lys Lys Val Asn Ile Ile Thr Leu
405 410 415

Ala Glu Thr Gly Ser Leu Asp Phe Arg Thr Phe Cys Thr Ser Cys Leu
420 425 430

Ile Arg Lys Pro Leu Arg Ser Leu His Cys His Val Cys Asn Cys Cys
435 440 445

Val Ala Arg Tyr Asp Gln His Cys Leu Trp Thr Gly Arg Cys Ile Gly
450 455 460

Phe Gly Asn His His Tyr Tyr Ile Phe Phe Leu Phe Phe Leu Ser Met
465 470 475 480

Val Cys Gly Trp Ile Ile Tyr Gly Ser Phe Ile Tyr Leu Ser Ser His
485 490 495

Cys Ala Thr Thr Phe Lys Glu Asp Gly Leu Trp Thr Tyr Leu Asn Gln
500 505 510

Ile Val Ala Cys Ser Pro Trp Val Leu Tyr Ile Leu Met Leu Ala Thr
515 520 525

Phe His Phe Ser Trp Ser Thr Phe Leu Leu Leu Asn Gln Leu Phe Gln
530 535 540

Ile Ala Phe Leu Gly Leu Thr Ser His Glu Arg Ile Ser Leu Gln Lys
545 550 555 560

Gln Ser Lys His Met Lys Gln Thr Leu Ser Leu Arg Lys Thr Pro Tyr
565 570 575

Asn Leu Gly Phe Met Gln Asn Leu Ala Asp Phe Phe Gln Cys Gly Cys
580 585 590

Phe Gly Leu Val Lys Pro Cys Val Val Asp Trp Thr Ser Gln Tyr Thr
595 600 605

Met Val Phe His Pro Ala Arg Glu Lys Val Leu Arg Ser Val
610 615 620

<210> 54

<211> 2426

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (104).. (1969)

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gctacttgcc tagtagcctc agccgctgtg ggctcctggg gag atg gag ggg ccg 115

Met Glu Gly Pro

1

ggg ctg ggc tcg cag tgc agg aat cac agc cat ggc ccc cac cct cca 163

Gly Leu Gly Ser Gln Cys Arg Asn His Ser His Gly Pro His Pro Pro

5

10

15

20

gga ttt ggt cga tat ggc atc tgt gca cat gaa aac aaa gaa ctt gcc 211

Gly Phe Gly Arg Tyr Gly Ile Cys Ala His Glu Asn Lys Glu Leu Ala

25

30

35

aat gca aga gaa gct ctt cct ctt ata gag gac tct agt aac tgt gac 259

Asn Ala Arg Glu Ala Leu Pro Leu Ile Glu Asp Ser Ser Asn Cys Asp

40

45

50

att gtc aaa gct act caa tac gga att ttt gaa cga tgt aaa gag ttg 307

Ile Val Lys Ala Thr Gln Tyr Gly Ile Phe Glu Arg Cys Lys Glu Leu

55

60

65

gta gaa gca gga tat gat gtc agg caa cca gat aaa gaa aat gtg tcg 355

Val Glu Ala Gly Tyr Asp Val Arg Gln Pro Asp Lys Glu Asn Val Ser

70

75

80

ctt ctt cat tgg gct gct att aac aac aga ctg gat ctt gta aag ttt 403

Leu Leu His Trp Ala Ala Ile Asn Asn Arg Leu Asp Leu Val Lys Phe

85

90

95

100

tat att tca aaa ggt gct gtt gta gat cag ttg ggt gga gat tta aat 451

Tyr Ile Ser Lys Gly Ala Val Val Asp Gln Leu Gly Gly Asp Leu Asn

105

110

115

tca act cct ctt cac tgg gcc atc cga caa gga cat tta cct atg gtc 499

Ser Thr Pro Leu His Trp Ala Ile Arg Gln Gly His Leu Pro Met Val

120

125

130

ata tta tta ctc cag cat ggt gca gac ccc act ctt att gat gga gag 547

Ile Leu Leu Leu Gln His Gly Ala Asp Pro Thr Leu Ile Asp Gly Glu

135

140

145

gga ttc agc agc atc cac ctg gca gta ttg ttt caa cac atg cct att 595

Gly Phe Ser Ser Ile His Leu Ala Val Leu Phe Gln His Met Pro Ile

150

155

160

ata gca tat ctc atc tca aag gga cag agt gtg aat atg aca gat gta 643

Ile Ala Tyr Leu Ile Ser Lys Gly Gln Ser Val Asn Met Thr Asp Val

165

170

175

180

aat ggg cag aca cct ctc atg tta tca gct cac aaa gta att ggg cca 691

Asn Gly Gln Thr Pro Leu Met Leu Ser Ala His Lys Val Ile Gly Pro

185

190

195

gaa cca act gga ttt ctt tta aag ttt aat cct tct ctc aat gtg gtt 739

Glu Pro Thr Gly Phe Leu Leu Lys Phe Asn Pro Ser Leu Asn Val Val

200

205

210

gat aaa ata cac caa aac act cca ctt cac tgg gca gtt gca gca gga 787

Asp Lys Ile His Gln Asn Thr Pro Leu His Trp Ala Val Ala Ala Gly

215	220	225	
aat gtt aat gca gtt gat aag ctt ttg gaa gct ggt tct agc ctg gat 835			
Asn Val Asn Ala Val Asp Lys Leu Leu Glu Ala Gly Ser Ser Leu Asp			
230	235	240	
atc cag aat gtt aag gga gaa aca cct ctt gat atg gct cta caa aac 883			
Ile Gln Asn Val Lys Gly Glu Thr Pro Leu Asp Met Ala Leu Gln Asn			
245	250	255	260
aaa aat cag ctc att att cat atg cta aaa aca gaa gcc aaa atg aga 931			
Lys Asn Gln Leu Ile Ile His Met Leu Lys Thr Glu Ala Lys Met Arg			
265	270	275	
gcc aac caa aag ttc aga ctt tgg agg tgg ctg cag aaa tgc gag ctc 979			
Ala Asn Gln Lys Phe Arg Leu Trp Arg Trp Leu Gln Lys Cys Glu Leu			
280	285	290	
ttc ctg ctg ctg atg ctt tct gtg att acc atg tgg gct att gga tac 1027			
Phe Leu Leu Leu Met Leu Ser Val Ile Thr Met Trp Ala Ile Gly Tyr			
295	300	305	
ata ttg gac ttc aat tca gat tct tgg ctt tta aaa gga tgt ctt cta 1075			
Ile Leu Asp Phe Asn Ser Asp Ser Trp Leu Leu Lys Gly Cys Leu Leu			
310	315	320	
gta aca ctg ttt ttt ctg aca tct ttg ttt cca agg ttc ttg gtt ggg 1123			
Val Thr Leu Phe Phe Leu Thr Ser Leu Phe Pro Arg Phe Leu Val Gly			
325	330	335	340

tat aag aac ctt gta tac tta cca aca gcc ttt ctg cta agt tct gtt 1171

Tyr Lys Asn Leu Val Tyr Leu Pro Thr Ala Phe Leu Leu Ser Ser Val

345

350

355

ttt tgg ata ttt atg act tgg ttc atc tta ttt ttt cct gat tta gca 1219

Phe Trp Ile Phe Met Thr Trp Phe Ile Leu Phe Phe Pro Asp Leu Ala

360

365

370

gga gcc cct ttc tat ttc agt ttc att ttc agc ata gta gcc ttt cta 1267

Gly Ala Pro Phe Tyr Phe Ser Phe Ile Phe Ser Ile Val Ala Phe Leu

375

380

385

tac ttt ttc tat aag act tgg gca act gat cca ggc ttc act aag gct 1315

Tyr Phe Phe Tyr Lys Thr Trp Ala Thr Asp Pro Gly Phe Thr Lys Ala

390

395

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tct gaa gaa gaa aag aaa gtg aat atc atc acc ctt gca gaa act ggc 1363

Ser Glu Glu Glu Lys Lys Val Asn Ile Ile Thr Leu Ala Glu Thr Gly

405

410

415

420

tct ctg gac ttc aga aca ttt tgt aca tca tgt ctt ata agg aag cca 1411

Ser Leu Asp Phe Arg Thr Phe Cys Thr Ser Cys Leu Ile Arg Lys Pro

425

430

435

tta agg tca ctc cac tgc cat gta tgc aac tgc tgt gtg gct cga tat 1459

Leu Arg Ser Leu His Cys His Val Cys Asn Cys Cys Val Ala Arg Tyr

440

445

450

gat caa cac tgc ctg tgg act gga cgg tgc ata ggt ttt ggc aac cat 1507

Asp Gln His Cys Leu Trp Thr Gly Arg Cys Ile Gly Phe Gly Asn His

455

460

465

cac tat tac ata ttc ttc ttg ttt ttc ctt tcc atg gta tgt ggc tgg 1555

His Tyr Tyr Ile Phe Phe Leu Phe Phe Leu Ser Met Val Cys Gly Trp

470

475

480

att ata tat gga tct ttc atc tat ttg tcc agt cat tgt gcc aca aca 1603

Ile Ile Tyr Gly Ser Phe Ile Tyr Leu Ser Ser His Cys Ala Thr Thr

485

490

495

500

ttc aaa gaa gat gga tta tgg act tac ctc aat cag att gtg gcc tgt 1651

Phe Lys Glu Asp Gly Leu Trp Thr Tyr Leu Asn Gln Ile Val Ala Cys

505

510

515

tcc cct tgg gtt tta tat atc ttg atg cta gca act ttc cat ttc tca 1699

Ser Pro Trp Val Leu Tyr Ile Leu Met Leu Ala Thr Phe His Phe Ser

520

525

530

tgg tca aca ttt tta tta tta aat caa ctc ttt cag att gcc ttt ctg 1747

Trp Ser Thr Phe Leu Leu Leu Asn Gln Leu Phe Gln Ile Ala Phe Leu

535

540

545

ggc ctg acc tcc cat gag aga atc agc ctg cag aag cag agc aag cat 1795

Gly Leu Thr Ser His Glu Arg Ile Ser Leu Gln Lys Gln Ser Lys His

550

555

560

atg aaa cag acg ttg tcc ctc agg aag aca cca tac aat ctt gga ttc 1843

Met Lys Gln Thr Leu Ser Leu Arg Lys Thr Pro Tyr Asn Leu Gly Phe

565 570 575 580

atg cag aac ctg gca gat ttc ttt cag tgt ggc tgc ttt ggc ttg gtg 1891

Met Gln Asn Leu Ala Asp Phe Phe Gln Cys Gly Cys Phe Gly Leu Val

585 590 595

aag ccc tgt gtg gta gat tgg aca tca cag tac acc atg gtc ttt cac 1939

Lys Pro Cys Val Val Asp Trp Thr Ser Gln Tyr Thr Met Val Phe His

600 605 610

cca gcc agg gag aag gtt ctt cgc tca gta tgaagaaaag caacccaaaa 1989

Pro Ala Arg Glu Lys Val Leu Arg Ser Val

615 620

ctctcaatct gatttgTTTT tgTTTatgtc gatgcCctgt agTTtgaaag tgaagtaaag 2049

atttagaatt cacctaagtc caaaggaaaa cacgtggTTT ttaaagccat taggtaaaaa 2109

aagttctcaa taaaggcatt acaattTTTT aggttttagaa agatggactt ttctgataaa 2169

tcttggcaga catctaaaaa aaaaaccata tttttcacaa gaaaatgcaa gttactTTTT 2229

ttggaaataa tactcactga ttatggataa aatggaatat tticagatac tatattggct 2289

gtttcaaaat agtactattc tttaaacttg taatttttgc taagttattt gtctttgttg 2349

tatctataaa tatgtaaaaa atatttaa atagatgtacct gttttgcttt cacactta at 2409

aaaaaatttt tttttgt

2426

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<211> 257

<212> PRT

<213> Homo sapiens

<400> 55

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Gln Leu Gly Ser Val Leu Leu Thr Arg Cys Pro Phe Trp Gly Cys Phe

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Ser Gln Leu Met Leu Tyr Ala Glu Arg Ala Glu Ala Arg Arg Lys Pro

35 40 45

Asp Ile Pro Val Pro Tyr Leu Tyr Phe Asp Met Gly Ala Ala Val Leu

50 55 60

Cys Ala Ser Phe Met Ser Phe Gly Val Lys Arg Arg Trp Phe Ala Leu

65 70 75 80

Gly Ala Ala Leu Gln Leu Ala Ile Ser Thr Tyr Ala Ala Tyr Ile Gly

85 90 95

Gly Tyr Val His Tyr Gly Asp Trp Leu Lys Val Arg Met Tyr Ser Arg

100 105 110

176/735

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<211> 1520
<212> DNA
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atc atg cag ttg ggt tcg gtg ctg ctc aca cgc tgc ccc ttt tgg ggc 99
Ile Met Gln Leu Gly Ser Val Leu Leu Thr Arg Cys Pro Phe Trp Gly
15 20 25 30

tgc ttc agc cag ctc atg ctg tac gct gag agg gct gag gca cgc cgg 147
Cys Phe Ser Gln Leu Met Leu Tyr Ala Glu Arg Ala Glu Ala Arg Arg
35 40 45

aag ccc gac atc cca gtg cct tac ctg tat ttc gac atg ggg gca gcc 195
Lys Pro Asp Ile Pro Val Pro Tyr Leu Tyr Phe Asp Met Gly Ala Ala
50 55 60

Gly Gly Glu Leu Met Ile Gln Leu Phe Phe Val Leu Tyr Gly Ile Leu
175 180 185 190

gcc ctg gcc ttt ctg tca ggc tac tac gtg acc ctc gct gcc cag atc 627
Ala Leu Ala Phe Leu Ser Gly Tyr Tyr Val Thr Leu Ala Ala Gln Ile
195 200 205

ctg gct gta ctg ctg ccc cct gtc atg ctg ctc att gat ggc aat gtt 675
Leu Ala Val Leu Leu Pro Pro Val Met Leu Leu Ile Asp Gly Asn Val
210 215 220

gct tac tgg cac aac acg cgg cgt gtt gag ttc tgg aac cag atg aag 723
Ala Tyr Trp His Asn Thr Arg Arg Val Glu Phe Trp Asn Gln Met Lys
225 230 235

ctc ctt gga gag agt gtg ggc atc ttc gga act gct gtc atc ctg gcc 771
Leu Leu Gly Glu Ser Val Gly Ile Phe Gly Thr Ala Val Ile Leu Ala
240 245 250

act gat ggc tgagttttat ggcaagaggc tgagatgggc acagggagcc 820
Thr Asp Gly
255

actgagggtc accctgcett cctccttgct ggcccagctg ctgtttatth atgttttttg 880

gtctgtttgt ttgatctttt gcttttttaa aattgttttt tgcagttaag aggcagctca 940

tttgtccaaa tttctgggct cagcgcttgg gagggcagga gccctggcac taatgctgta 1000

caggtttttt tcctgttagg agagctgagg ccagctgccc actgagtctc ctgtccctga 1060

gaagggagta tggcagggct gggatgcggc tactgagagt gggagagtgg gagacagagg 1120

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gcagctaggc tctgcagtgc tgtttggaga ctgtgagagg gagtgtgtgt gttgacacat 1240

gtggatcagg cccaggaagg gcacaggggc tgagcactac agaagtcaca tgggttctca 1300

gggtatgcca ggggcagaaa cagtaccggc tctctgtcac tcaccttgag agtagagcag 1360

accctgttct gctctgggct gtgaaggggt ggagcaggca gtggccagct ttgcccttcc 1420

tgctgtctct gtttctagct ccatggttgg cctgggtggg gtggagttcc ctcccaaaca 1480

ccagaccaca cagtctctca aaaataaaca ttttatatag 1520

<210> 57

<211> 107

<212> PRT

<213> Homo sapiens

<400> 57

Met Ala Leu Phe Ala Gly Gly Lys Leu Arg Val His Leu Asp Ile Gln

1

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Val Gly Glu His Ala Asn Asn Tyr Pro Glu Ile Ala Ala Lys Asp Lys

.. .. .

20

25

30

Leu Thr Glu Leu Gln Leu Arg Ala Arg Gln Leu Leu Asp Gln Val Glu

35

40

45

Gln Ile Gln Lys Glu Gln Asp Tyr Gln Arg Tyr Arg Glu Glu Arg Phe

50

55

60

Arg Leu Thr Ser Glu Ser Thr Asn Gln Arg Val Leu Trp Trp Ser Ile

65

70

75

80

Ala Gln Thr Val Ile Leu Ile Leu Thr Gly Ile Trp Gln Met Arg His

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90

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Leu Lys Ser Phe Phe Glu Ala Lys Lys Leu Val

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<210> 58

<211> 1496

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (9).. (329)

<400> 58

ctaccagg atg gct ctc ttc gct ggt ggc aaa ctg cgt gtg cat ctc gac 50

182/735

Met Ala Leu Phe Ala Gly Gly Lys Leu Arg Val His Leu Asp

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5

10

atc cag gtt ggg gag cat gcc aac aac tac cct gag att gct gca aaa 98

Ile Gln Val Gly Glu His Ala Asn Asn Tyr Pro Glu Ile Ala Ala Lys

15

20

25

30

gat aag ctg acg gag cta cag ctc cgc gcc cgc cag ttg ctt gat cag 146

Asp Lys Leu Thr Glu Leu Gln Leu Arg Ala Arg Gln Leu Leu Asp Gln

35

40

45

gtg gaa cag att cag aag gag cag gat tac caa agg tat cgt gaa gag 194

Val Glu Gln Ile Gln Lys Glu Gln Asp Tyr Gln Arg Tyr Arg Glu Glu

50

55

60

cgc ttc cga ctg acg agc gag agc acc aac cag agg gtc cta tgg tgg 242

Arg Phe Arg Leu Thr Ser Glu Ser Thr Asn Gln Arg Val Leu Trp Trp

65

70

75

tcc att gct cag act gtc atc ctc atc ctc act ggc atc tgg cag atg 290

Ser Ile Ala Gln Thr Val Ile Leu Ile Leu Thr Gly Ile Trp Gln Met

80

85

90

cgt cac ctc aag agc ttc ttt gag gcc aag aag ctg gtg tagtgccctc 339

Arg His Leu Lys Ser Phe Phe Glu Ala Lys Lys Leu Val

95

100

105

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ccacctggat ttttagggaa aaaaaatgaa aaagaataag tcacattggt tccatggcca 459

caaaccattc agatcagcca ctgtctgacc ctggttctta aggacacatg acattagtcc 519

aatctttcaa aatcttgtct tagggcttgt gaggaatcag aactaaccca ggactcagtc 579

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acagagcagg cctgcctca ctgtctgctg gtcagttctg ggttcactta atggctttgt 759

gaatgtaaat aaggggcagg tcttgccct agaggattga gatgtttttc tatatcttag 819

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ataaaacatg ttgtaat 1496

<210> 59

<211> 272

<212> PRT

<213> Homo sapiens

<400> 59

Met Met Ile His Gly Phe Gln Ser Ser His Arg Asp Phe Cys Phe Gly

1 5 10 15

Pro Trp Lys Leu Thr Ala Ser Lys Thr His Ile Met Lys Ser Ala Asp

20 25 30

Val Glu Lys Leu Ala Asp Glu Leu His Met Pro Ser Leu Pro Glu Met

35 40 45

Met Phe Gly Asp Asn Val Leu Arg Ile Gln His Gly Ser Gly Phe Gly

50 55 60

Ile Glu Phe Asn Ala Thr Asp Ala Leu Arg Cys Val Asn Asn Tyr Gln

65 70 75 80

Gly Met Leu Lys Val Ala Cys Ala Glu Glu Trp Gln Glu Ser Arg Thr

85 90 95

Glu Gly Glu His Ser Lys Glu Val Ile Lys Pro Tyr Asp Trp Thr Tyr

100 105 110

Thr Thr Asp Tyr Lys Gly Thr Leu Leu Gly Glu Ser Leu Lys Leu Lys

115 120 125

Val Val Pro Thr Thr Asp His Ile Asp Thr Glu Lys Leu Lys Ala Arg

130 135 140

Glu Gln Ile Lys Phe Phe Glu Glu Val Leu Leu Phe Glu Asp Glu Leu

145 150 155 160

His Asp His Gly Val Ser Ser Leu Ser Val Lys Ile Arg Val Met Pro

165 170 175

Ser Ser Phe Phe Leu Leu Leu Arg Phe Phe Leu Arg Ile Asp Gly Val

180 185 190

Leu Ile Arg Met Asn Asp Thr Arg Leu Tyr His Glu Ala Asp Lys Thr

195 200 205

Tyr Met Leu Arg Glu Tyr Thr Ser Arg Glu Ser Lys Ile Ser Ser Leu

210 215 220

tgg aag ctg acg gcg tcc aag acc cac atc atg aag tcg gcg gat gtg 215

Trp Lys Leu Thr Ala Ser Lys Thr His Ile Met Lys Ser Ala Asp Val

20

25

30

gag aaa tta gcc gat gaa tta cat atg cca tct ctc cct gaa atg atg 263

Glu Lys Leu Ala Asp Glu Leu His Met Pro Ser Leu Pro Glu Met Met

35

40

45

ttt gga gac aac gtt tta aga atc cag cat ggg tct ggc ttt gga att 311

Phe Gly Asp Asn Val Leu Arg Ile Gln His Gly Ser Gly Phe Gly Ile

50

55

60

65

gag ttc aat gct aca gat gcg tta aga tgt gta aac aac tac caa gga 359

Glu Phe Asn Ala Thr Asp Ala Leu Arg Cys Val Asn Asn Tyr Gln Gly

70

75

80

atg ctt aaa gtg gcc tgt gct gaa gag tgg caa gaa agc agg acg gag 407

Met Leu Lys Val Ala Cys Ala Glu Glu Trp Gln Glu Ser Arg Thr Glu

85

90

95

ggt gaa cac tcc aaa gag gtt att aaa cca tat gat tgg acc tat aca 455

Gly Glu His Ser Lys Glu Val Ile Lys Pro Tyr Asp Trp Thr Tyr Thr

100

105

110

aca gat tat aag gga acc tta ctt gga gaa tct ctt aag tta aag gtt 503

Thr Asp Tyr Lys Gly Thr Leu Leu Gly Glu Ser Leu Lys Leu Lys Val

115

120

125

gta cct aca aca gat cat ata gat aca gaa aaa ttg aaa gcc aga gaa 551

Val Pro Thr Thr Asp His Ile Asp Thr Glu Lys Leu Lys Ala Arg Glu

130 135 140 145

cag att aag ttt ttt gaa gaa gtt ctc ctt ttt gag gat gaa ctt cat 599

Gln Ile Lys Phe Phe Glu Glu Val Leu Leu Phe Glu Asp Glu Leu His

150 155 160

gat cat gga gtt tca agc ctg agt gtg aag att aga gta atg cct tct 647

Asp His Gly Val Ser Ser Leu Ser Val Lys Ile Arg Val Met Pro Ser

165 170 175

agc ttt ttc ctg ctg ttg cgg ttt ttc ttg aga att gat ggg gtg ctt 695

Ser Phe Phe Leu Leu Leu Arg Phe Phe Leu Arg Ile Asp Gly Val Leu

180 185 190

atc aga atg aat gac acg aga ctt tac cat gag gct gac aag acc tac 743

Ile Arg Met Asn Asp Thr Arg Leu Tyr His Glu Ala Asp Lys Thr Tyr

195 200 205

atg tta cga gaa tat acg tca cga gaa agc aaa att tct agt ttg atg 791

Met Leu Arg Glu Tyr Thr Ser Arg Glu Ser Lys Ile Ser Ser Leu Met

210 215 220 225

cat gtt cca cct tcc ctc ttc acg gaa cct aat gaa ata tcc cag tat 839

His Val Pro Pro Ser Leu Phe Thr Glu Pro Asn Glu Ile Ser Gln Tyr

230 235 240

tta cca ata aag gaa gca gtt tgt gag aag cta ata ttt cca gaa aga 887

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250

gtgtgtgtgt gtgtgtgtgt gtgtatacag actttttttt ttaacttggt gattcagatg 1652

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ggaattaaaa taattgcctt ttttttttta gagggtaaga gatgggtaga agagtatgcc 1772

tctgaaaatt ttattagttt attcttgtgg agaataccaa gaaaatgtgt atttgcccat 1832

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agaataaaca ataaggaatt actg 1916

<210> 61

<211> 219

<212> PRT

<213> Homo sapiens

<400> 61

Met Asn Arg Leu Phe Gly Lys Ala Lys Pro Lys Ala Pro Pro Pro Ser

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Leu Thr Asp Cys Ile Gly Thr Val Asp Ser Arg Ala Glu Ser Ile Asp

20

25

30

Lys Lys Ile Ser Arg Leu Asp Ala Glu Leu Val Lys Tyr Lys Asp Gln

35

40

45

Ile Lys Lys Met Arg Glu Gly Pro Ala Lys Asn Met Val Lys Gln Lys

... ..

50

55

60

Ala Leu Arg Val Leu Lys Gln Lys Arg Met Tyr Glu Gln Gln Arg Asp

65

70

75

80

Asn Leu Ala Gln Gln Ser Phe Asn Met Glu Gln Ala Asn Tyr Thr Ile

85

90

95

Gln Ser Leu Lys Asp Thr Lys Thr Thr Val Asp Ala Met Lys Leu Gly

100

105

110

Val Lys Glu Met Lys Lys Ala Tyr Lys Gln Val Lys Ile Asp Gln Ile

115

120

125

Glu Asp Leu Gln Asp Gln Leu Glu Asp Met Met Glu Asp Ala Asn Glu

130

135

140

Ile Gln Glu Ala Leu Ser Arg Ser Tyr Gly Thr Pro Glu Leu Asp Glu

145

150

155

160

Asp Asp Leu Glu Ala Glu Leu Asp Ala Leu Gly Asp Glu Leu Leu Ala

165

170

175

Asp Glu Asp Ser Ser Tyr Leu Asp Glu Ala Ala Ser Ala Pro Ala Ile

180

185

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Pro Glu Gly Val Pro Thr Asp Thr Lys Asn Lys Asp Gly Val Leu Val

195

200

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Asp Glu Phe Gly Leu Pro Gln Ile Pro Ala Ser
210 215

<210> 62
<211> 1362
<212> DNA
<213> Homo sapiens

<220>
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<222> (49).. (705)

<400> 62
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Met Asn Arg
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ctc ttc ggg aaa gcg aaa ccc aag gct ccg ccg ccc agc ctg act gac 105
Leu Phe Gly Lys Ala Lys Pro Lys Ala Pro Pro Pro Ser Leu Thr Asp
5 10 15

tgc att ggc acg gtg gac agt aga gca gaa tcc att gac aag aag att 153
Cys Ile Gly Thr Val Asp Ser Arg Ala Glu Ser Ile Asp Lys Lys Ile
20 25 30 35

tct cga ttg gat gct gag cta gtg aag tat aag gat cag atc aag aag 201
Ser Arg Leu Asp Ala Glu Leu Val Lys Tyr Lys Asp Gln Ile Lys Lys
40 45 50

atg aga gag ggt cct gca aag aat atg gtc aag cag aaa gcc ttg cga 249

Met Arg Glu Gly Pro Ala Lys Asn Met Val Lys Gln Lys Ala Leu Arg

55

60

65

gtt tta aag caa aag agg atg tat gag cag cag cgg gac aat ctt gcc 297

Val Leu Lys Gln Lys Arg Met Tyr Glu Gln Gln Arg Asp Asn Leu Ala

70

75

80

caa cag tca ttc aac atg gaa caa gcc aat tat acc atc cag tct ttg 345

Gln Gln Ser Phe Asn Met Glu Gln Ala Asn Tyr Thr Ile Gln Ser Leu

85

90

95

aag gac acc aag acc acg gtt gat gct atg aaa ctg gga gta aag gaa 393

Lys Asp Thr Lys Thr Thr Val Asp Ala Met Lys Leu Gly Val Lys Glu

100

105

110

115

atg aag aag gca tac aag caa gtg aag atc gac cag att gag gat tta 441

Met Lys Lys Ala Tyr Lys Gln Val Lys Ile Asp Gln Ile Glu Asp Leu

120

125

130

caa gac cag cta gag gat atg atg gaa gat gca aat gaa atc caa gaa 489

Gln Asp Gln Leu Glu Asp Met Met Glu Asp Ala Asn Glu Ile Gln Glu

135

140

145

gca ctg agt cgc agt tat ggc acc cca gaa ctg gat gaa gat gat tta 537

Ala Leu Ser Arg Ser Tyr Gly Thr Pro Glu Leu Asp Glu Asp Asp Leu

150

155

160

agt tct tat ttg gat gag gca gca tct gca cct gca att cca gaa ggt 633
 ser ser tyr leu asp glu ala ala ser ala pro ala ile pro glu gly
 180 185 190 195

gtt ccc act gat aca aaa aac aag gat gga gtt ctg gtg gat gaa ttt 681
 val pro thr asp thr lys asn lys asp gly val leu val asp glu phe
 200 205 210

gga ttg cca cag atc cct gct tca tagatttgca tcattcaage atatcttgta 735
 gly leu pro gln ile pro ala ser
 215

aaacaaacac atattatggg actaggaaat atttatcttt ccaaatttgc cataacagat 795

ttaggtttct ttcctttctt tgaaggaaag tttaattaca ttgctctttt attttttcca 855

ttaagagact cattgcttgg gaaatgcttt ctctgtacta aaatttgatt cttttttttt 915

cttatgaaaa acgaactcag tttaaaagta ttttttagctc gtatgacttg ttttcattca 975

ttaataataa ttgaaataa aactaaggaa atggaatctt aaaagtctat gacagtgtaa 1035

ctctacagtc tcaaatgac ctgataaatt gataagacaa agatgagatt attggggctg 1095

ttcattattat gattcagaat cattttctat tgtgggtatta taggttggtt aaagtgatgg 1155



Ser Val Ala Leu Phe Tyr Asn Phe Gly Lys Ser Trp Lys Ser Asp Pro
385 390 395 400

Gly Ile Ile Lys Ala Thr Glu Glu Gln Lys Lys Lys Thr Ile Val Glu
405 410 415

Leu Ala Glu Thr Gly Ser Leu Asp Leu Ser Ile Phe Cys Ser Thr Cys
420 425 430

Leu Ile Arg Lys Pro Val Arg Ser Lys His Cys Gly Val Cys Asn Arg
435 440 445

Cys Ile Ala Lys Phe Asp His His Cys Pro Trp Val Gly Asn Cys Val
450 455 460

Gly Ala Gly Asn His Arg Tyr Phe Met Gly Tyr Leu Phe Phe Leu Leu
465 470 475 480

Phe Met Ile Cys Trp Met Ile Tyr Gly Cys Ile Ser Tyr Trp Gly Leu
485 490 495

His Cys Glu Thr Thr Tyr Thr Lys Asp Gly Phe Trp Thr Tyr Ile Thr
500 505 510

Gln Ile Ala Thr Cys Ser Pro Trp Met Phe Trp Met Phe Leu Asn Ser
515 520 525

Val Phe His Phe Met Trp Val Ala Val Leu Leu Met Cys Gln Met Tyr
199/735

530

535

540

Gln Ile Ser Cys Leu Gly Ile Thr Thr Asn Glu Arg Met Asn Ala Arg

545

550

555

560

Arg Tyr Lys His Phe Lys Val Thr Thr Thr Ser Ile Glu Ser Pro Phe

565

570

575

Asn His Gly Cys Val Arg Asn Ile Ile Asp Phe Phe Glu Phe Arg Cys

580

585

590

Cys Gly Leu Phe Arg Pro Val Ile Val Asp Trp Thr Arg Gln Tyr Thr

595

600

605

Ile Glu Tyr Asp Gln Ile Ser Gly Ser Gly Tyr Gln Leu Val

610

615

620

<210> 64

<211> 2948

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (14)..(1879)

<400> 64

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ggc tgt gtg ccc ctt ctc cac cca gag gaa atc aaa ccc caa agc cat 97

Gly Cys Val Pro Leu Leu His Pro Glu Glu Ile Lys Pro Gln Ser His

15 20 25

tat aac cat gga tat ggt gaa cct ctt gga cgg aaa act cat att gat 145

Tyr Asn His Gly Tyr Gly Glu Pro Leu Gly Arg Lys Thr His Ile Asp

30 35 40

gat tac agc aca tgg gac ata gtc aag gct aca caa tat gga ata tat 193

Asp Tyr Ser Thr Trp Asp Ile Val Lys Ala Thr Gln Tyr Gly Ile Tyr

45 50 55 60

gaa cgc tgt cga gaa ttg gtg gaa gca ggt tat gat gta cgg caa ccg 241

Glu Arg Cys Arg Glu Leu Val Glu Ala Gly Tyr Asp Val Arg Gln Pro

65 70 75

gac aaa gaa aat gtt acc ctc ctc cat tgg gct gcc atc aat aac aga 289

Asp Lys Glu Asn Val Thr Leu Leu His Trp Ala Ala Ile Asn Asn Arg

80 85 90

ata gat tta gtc aaa tac tat att tcg aaa ggt gct att gtg gat caa 337

Ile Asp Leu Val Lys Tyr Tyr Ile Ser Lys Gly Ala Ile Val Asp Gln

95 100 105

ctt gga ggg gac ctg aat tca act cca ttg cac tgg gcc aca aga caa 385

Leu Gly Gly Asp Leu Asn Ser Thr Pro Leu His Trp Ala Thr Arg Gln

120

gct gga gct aat gtt gat gcc cag aat atc aag ggc gaa tca gcg ctt 769
 Ala Gly Ala Asn Val Asp Ala Gln Asn Ile Lys Gly Glu Ser Ala Leu
 240 245 250

gat ttg gca aaa cag aga aaa aat gtg tgg atg atc aac cac tta caa 817
 Asp Leu Ala Lys Gln Arg Lys Asn Val Trp Met Ile Asn His Leu Gln
 255 260 265

gag gca agg caa gca aaa gga tat gac aat ccg tcc ttc ctt aga aag 865
 Glu Ala Arg Gln Ala Lys Gly Tyr Asp Asn Pro Ser Phe Leu Arg Lys
 270 275 280

ctg aaa gct gat aag gaa ttt cgg cag aaa gta atg tta gga act cct 913
 Leu Lys Ala Asp Lys Glu Phe Arg Gln Lys Val Met Leu Gly Thr Pro
 285 290 295 300

ttc cta gtt att tgg ctg gtt ggg ttt ata gca gac cta aat att gat 961
 Phe Leu Val Ile Trp Leu Val Gly Phe Ile Ala Asp Leu Asn Ile Asp
 305 310 315

tct tgg ctc att aaa ggg cta atg tat ggt ggt gtt tgg gct aca gta 1009
 Ser Trp Leu Ile Lys Gly Leu Met Tyr Gly Gly Val Trp Ala Thr Val
 320 325 330

cag ttt ctt tca aaa tcc ttt ttc gat cat tca atg cat agt gca ttg 1057
 Gln Phe Leu Ser Lys Ser Phe Phe Asp His Ser Met His Ser Ala Leu
 335 340 345

ccc ctt ggg ata tat ttg gca acc aaa ttc tgg atg tat gtg acg tgg 1105

Pro Leu Gly Ile Tyr Leu Ala Thr Lys Phe Trp Met Tyr Val Thr Trp

350

355

360

ttc ttc tgg ttt tgg aat gat ctc aac ttt tta ttt atc cat ctt cca 1153

Phe Phe Trp Phe Trp Asn Asp Leu Asn Phe Leu Phe Ile His Leu Pro

365

370

375

380

ttc ctt gcc aat agt gtt gca ctt ttc tac aat ttt gga aaa tct tgg 1201

Phe Leu Ala Asn Ser Val Ala Leu Phe Tyr Asn Phe Gly Lys Ser Trp

385

390

395

aaa tca gat cca ggg att att aaa gca aca gaa gag caa aag aaa aag 1249

Lys Ser Asp Pro Gly Ile Ile Lys Ala Thr Glu Glu Gln Lys Lys Lys

400

405

410

aca ata gtt gaa ctt gca gag aca gga agt ctg gac ctc agt ata ttc 1297

Thr Ile Val Glu Leu Ala Glu Thr Gly Ser Leu Asp Leu Ser Ile Phe

415

420

425

tgc agt acc tgt ttg ata cga aaa ccg gtg agg tcc aaa cat tgt ggt 1345

Cys Ser Thr Cys Leu Ile Arg Lys Pro Val Arg Ser Lys His Cys Gly

430

435

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gtg tgc aac cgc tgt ata gca aaa ttt gat cat cat tgc cca tgg gtg 1393

Val Cys Asn Arg Cys Ile Ala Lys Phe Asp His His Cys Pro Trp Val

445

450

455

460

ggc aac tgt gta ggt gca ggc aac cat aga tat ttt atg ggc tac cta 1441



585

600

620

Leu Val

tttcagaatg tacacataaa tactgtgatg aaaatcatgt gattggggatc tactgtgatg 2409

ttgtcttcaa aggcaggaga aaataatggt cacaataaaa tgtgctaaca atgttttggt 2469

tctatcagct gttgcaatgc tgatatattt ctagttcagt gaaataattt gtagtaacct 2529

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ttttgttcaa atttaaaagc cctgctaatt gcatgacaca ccacatagaa tgtatactag 2649

cagatactat ccagtgaagc ataaattaga atttaatttg atgttcaaaa acagtccat 2709

ttttaagggt taagggtgta ttttcaagaa aaggcagaac aaataatgca aaattctcag 2769

taatagtgat acatggatat acttcctttt aaattctcag ctgcaaaata attgtagaca 2829

aaataatggc atttaactaa agatggagca tgatctgtgt acatagcaca tgtgaataaa 2889

agaaaagctg acagtatatt ctggtttcaa taaaatgacc tatcagaaag tagaatttc 2948

<210> 65

<211> 632

<212> PRT

<213> Homo sapiens

<400> 65

Met Gln Arg Glu Glu Gly Phe Asn Thr Lys Met Ala Asp Gly Pro Asp

1 5 10 15

Glu Tyr Asp Thr Glu Ala Gly Cys Val Pro Leu Leu His Pro Glu Glu

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20

25

30

Ile Lys Pro Gln Ser His Tyr Asn His Gly Tyr Gly Glu Pro Leu Gly

35

40

45

Arg Lys Thr His Ile Asp Asp Tyr Ser Thr Trp Asp Ile Val Lys Ala

50

55

60

Thr Gln Tyr Gly Ile Tyr Glu Arg Cys Arg Glu Leu Val Glu Ala Gly

65

70

75

80

Tyr Asp Val Arg Gln Pro Asp Lys Glu Asn Val Thr Leu Leu His Trp

85

90

95

Ala Ala Ile Asn Asn Arg Ile Asp Leu Val Lys Tyr Tyr Ile Ser Lys

100

105

110

Gly Ala Ile Val Asp Gln Leu Gly Gly Asp Leu Asn Ser Thr Pro Leu

115

120

125

His Trp Ala Thr Arg Gln Gly His Leu Ser Met Val Val Gln Leu Met

130

135

140

Lys Tyr Gly Ala Asp Pro Ser Leu Ile Asp Gly Glu Gly Cys Ser Cys

145

150

155

160

Ile His Leu Ala Ala Gln Phe Gly His Thr Ser Ile Val Ala Tyr Leu

165

170

175

Ile Ala Lys Gly Gln Asp Val Asp Met Met Asp Gln Asn Gly Met Thr

180

185

190

Pro Leu Met Trp Ala Ala Tyr Arg Thr His Ser Val Asp Pro Thr Arg

195

200

205

Leu Leu Leu Thr Phe Asn Val Ser Val Asn Leu Gly Asp Lys Tyr His

210

215

220

Lys Asn Thr Ala Leu His Trp Ala Val Leu Ala Gly Asn Thr Thr Val

225

230

235

240

Ile Ser Leu Leu Leu Glu Ala Gly Ala Asn Val Asp Ala Gln Asn Ile

245

250

255

Lys Gly Glu Ser Ala Leu Asp Leu Ala Lys Gln Arg Lys Asn Val Trp

260

265

270

Met Ile Asn His Leu Gln Glu Ala Arg Gln Ala Lys Gly Tyr Asp Asn

275

280

285

Pro Ser Phe Leu Arg Lys Leu Lys Ala Asp Lys Glu Phe Arg Gln Lys

290

295

300

Val Met Leu Gly Thr Pro Phe Leu Val Ile Trp Leu Val Gly Phe Ile

305

310

315

320

Ala Asp Leu Asn Ile Asp Ser Trp Leu Ile Lys Gly Leu Met Tyr Gly

325

330

335

.. .. .

Gly Val Trp Ala Thr Val Gln Phe Leu Ser Lys Ser Phe Phe Asp His

340

345

350

Ser Met His Ser Ala Leu Pro Leu Gly Ile Tyr Leu Ala Thr Lys Phe

355

360

365

Trp Met Tyr Val Thr Trp Phe Phe Trp Phe Trp Asn Asp Leu Asn Phe

370

375

380

Leu Phe Ile His Leu Pro Phe Leu Ala Asn Ser Val Ala Leu Phe Tyr

385

390

395

400

Asn Phe Gly Lys Ser Trp Lys Ser Asp Pro Gly Ile Ile Lys Ala Thr

405

410

415

Glu Glu Gln Lys Lys Lys Thr Ile Val Glu Leu Ala Glu Thr Gly Ser

420

425

430

Leu Asp Leu Ser Ile Phe Cys Ser Thr Cys Leu Ile Arg Lys Pro Val

435

440

445

Arg Ser Lys His Cys Gly Val Cys Asn Arg Cys Ile Ala Lys Phe Asp

450

455

460

His His Cys Pro Trp Val Gly Asn Cys Val Gly Ala Gly Asn His Arg

465

470

475

480

Tyr Phe Met Gly Tyr Leu Phe Phe Leu Leu Phe Met Ile Cys Trp Met

210/735

485

490

495

Ile Tyr Gly Cys Ile Ser Tyr Trp Gly Leu His Cys Glu Thr Thr Tyr

500

505

510

Thr Lys Asp Gly Phe Trp Thr Tyr Ile Thr Gln Ile Ala Thr Cys Ser

515

520

525

Pro Trp Met Phe Trp Met Phe Leu Asn Ser Val Phe His Phe Met Trp

530

535

540

Val Ala Val Leu Leu Met Cys Gln Met Tyr Gln Ile Ser Cys Leu Gly

545

550

555

560

Ile Thr Thr Asn Glu Arg Met Asn Ala Arg Arg Tyr Lys His Phe Lys

565

570

575

Val Thr Thr Thr Ser Ile Glu Ser Pro Phe Asn His Gly Cys Val Arg

580

585

590

Asn Ile Ile Asp Phe Phe Glu Phe Arg Cys Cys Gly Leu Phe Arg Pro

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Val Ile Val Asp Trp Thr Arg Gln Tyr Thr Ile Glu Tyr Asp Gln Ile

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Ser Gly Ser Gly Tyr Gln Leu Val

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630

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cctcgcctc gcccgagccc cgggagggtg aaacgctttc tcccagc atg cag cgg 116

Met Gln Arg

1

gag gag gga ttt aac acc aag atg gcg gac ggc ccg gat gag tac gat 164

Glu Glu Gly Phe Asn Thr Lys Met Ala Asp Gly Pro Asp Glu Tyr Asp

5

10

15

acc gaa gcg ggc tgt gtg ccc ctt ctc cac cca gag gaa atc aaa ccc 212

Thr Glu Ala Gly Cys Val Pro Leu Leu His Pro Glu Glu Ile Lys Pro

20

25

30

35

caa agc cat tat aac cat gga tat ggt gaa cct ctt gga cgg aaa act 260

Gln Ser His Tyr Asn His Gly Tyr Gly Glu Pro Leu Gly Arg Lys Thr

40

45

50

cat att gat gat tac agc aca tgg gac ata gtc aag gct aca caa tat 308

His Ile Asp Asp Tyr Ser Thr Trp Asp Ile Val Lys Ala Thr Gln Tyr

55

60

65

gga ata tat gaa cgc tgt cga gaa ttg gtg gaa gca ggt tat gat gta 356

Gly Ile Tyr Glu Arg Cys Arg Glu Leu Val Glu Ala Gly Tyr Asp Val

70

75

80

cgg caa ccg gac aaa gaa aat gtt acc ctc ctc cat tgg gct gcc atc 404

Arg Gln Pro Asp Lys Glu Asn Val Thr Leu Leu His Trp Ala Ala Ile

85

90

95

aat aac aga ata gat tta gtc aaa tac tat att tcg aaa ggt gct att 452

Asn Asn Arg Ile Asp Leu Val Lys Tyr Tyr Ile Ser Lys Gly Ala Ile

100

105

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gtg gat caa ctt gga ggg gac ctg aat tca act cca ttg cac tgg gcc 500

Val Asp Gln Leu Gly Gly Asp Leu Asn Ser Thr Pro Leu His Trp Ala

120

125

130

aca aga caa ggc cat cta tcc atg gtt gtg caa cta atg aaa tat ggt 548

Thr Arg Gln Gly His Leu Ser Met Val Val Gln Leu Met Lys Tyr Gly

135

140

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gca gat cct tca tta att gat gga gaa gga tgt agc tgt att cat ctg 596

Ala Asp Pro Ser Leu Ile Asp Gly Glu Gly Cys Ser Cys Ile His Leu

150

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gct gct cag ttc gga cat acc tca att gtt gct tat ctc ata gca aaa 644

Ala Ala Gln Phe Gly His Thr Ser Ile Val Ala Tyr Leu Ile Ala Lys

165

170

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gga cag gat gta gat atg atg gat cag aat gga atg acg cct tta atg 692

Gly Gln Asp Val Asp Met Met Asp Gln Asn Gly Met Thr Pro Leu Met

180

185

190

195

tgg gca gca tat aga aca cat agt gtg gat cca act aga ttg ctt tta 740

Trp Ala Ala Tyr Arg Thr His Ser Val Asp Pro Thr Arg Leu Leu Leu

200

205

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aca ttc aat gtt tca gtt aac ctt ggt gac aag tat cac aaa aac act 788

Thr Phe Asn Val Ser Val Asn Leu Gly Asp Lys Tyr His Lys Asn Thr

215

220

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gct ctg cat tgg gca gtg cta gca ggg aat acc aca gtc att agc ctt 836

Ala Leu His Trp Ala Val Leu Ala Gly Asn Thr Thr Val Ile Ser Leu

230

235

240

ctt ctg gaa gct gga gct aat gtt gat gcc cag aat atc aag ggc gaa 884

Leu Leu Glu Ala Gly Ala Asn Val Asp Ala Gln Asn Ile Lys Gly Glu

245

250

255

tca gcg ctt gat ttg gca aaa cag aga aaa aat gtg tgg atg atc aac 932

Ser Ala Leu Asp Leu Ala Lys Gln Arg Lys Asn Val Trp Met Ile Asn

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265

270

275

cac tta caa gag gca agg caa gca aaa gga tat gac aat ccg tcc ttc 980

His Leu Gln Glu Ala Arg Gln Ala Lys Gly Tyr Asp Asn Pro Ser Phe

214/735



415

435

450

465

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495

515

gga ttt tgg aca tac att act cag att gcc acg tgt tca cct tgg atg 1700

Gly Phe Trp Thr Tyr Ile Thr Gln Ile Ala Thr Cys Ser Pro Trp Met

520

525

530

ttt tgg atg ttc ctg aac agt gtt ttc cac ttc atg tgg gtg gct gta 1748

Phe Trp Met Phe Leu Asn Ser Val Phe His Phe Met Trp Val Ala Val

535

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545

tta ctc atg tgt cag atg tac cag ata tca tgt tta ggt att act aca 1796

Leu Leu Met Cys Gln Met Tyr Gln Ile Ser Cys Leu Gly Ile Thr Thr

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555

560

aat gaa aga atg aat gcc agg aga tac aag cac ttt aaa gtc aca aca 1844

Asn Glu Arg Met Asn Ala Arg Arg Tyr Lys His Phe Lys Val Thr Thr

565

570

575

acg tct att gaa agc cca ttc aac cat gga tgt gta aga aat att ata 1892

Thr Ser Ile Glu Ser Pro Phe Asn His Gly Cys Val Arg Asn Ile Ile

580

585

590

595

gac ttc ttt gaa ttt cga tgc tgt ggc ctc ttt cgt cct gtt atc gtg 1940

Asp Phe Phe Glu Phe Arg Cys Cys Gly Leu Phe Arg Pro Val Ile Val

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Asp Trp Thr Arg Gln Tyr Thr Ile Glu Tyr Asp Gln Ile Ser Gly Ser

615

620

625

ggg tac cag ctg gtg tagcgacatc ttatcctatg aagcatattg ctgagtggtg 2043

217/735

Gly Tyr Gln Leu Val

630

cctgaaaatt gtgtctgtcc gtgtctttct cacactcgaa tccacatcct ttgaacaaga 2103

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caaaagtaaa catggacaga acacactgcc atttctggga agagtaaaga tgataaaaaa 2223

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tactgtgatg ttgtcttcaa aggcaggaga aaataatgth cacaataaaa tgtgctaaca 2583

atgttttgth tctatcagct gttgcaatgc tgatatatth ctagttcagt gaaataatth 2643

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gcatatgtac tttatTTTTg aaaaggaag agatgggtgt ggggtggcaa tagcattgtg 3843

ccattttgtc atagaatgta aaaattgggtt aactttacaa atgtcagcta gttttgacta 3903

ctaattgggg gaaatttttag ataattttta aattcaaagt tatttataaa atgctagaat 3963

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aatacatttt tatcaacagt taaagactat ggtgggtttt tcagagtttg gctaagaatg 4083

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ttaaaaagac aaacctctag atgtgttaatt acatggaaaa tactagcaat gtgaatgctt 4203

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ggagccagct atgcagcagt ataccatctg ttttaattatt ttgtaggtcc tgttgtgtgga 4323

accaactata aaccagttc taaagttgtg tatgatgggtg aacctttggg aatagttctt 4383

atcaacttaa ttgatactt ttagcaaata ggaacttaat tctcagcact gaacatgaat 4443

tacttccttg gagttttttt tcattcatat ttttgttgtt tccaggaatt tatttgatat 4503

taatgggcgt aaaacagcat cattgtactt aagctatgga tgtttttatt ttatatatttc 4563

tttatttata actgtgccaa gtattatttt gctacttacc gtgttattct gtggaaagaa 4623

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taaaatatta atcagaataa atactgactc tt 4715

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<213> Homo sapiens

<400> 67

Met Ala Arg Leu Glu Val Ile Glu Leu Pro His Ser Pro Gln Asn Leu

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Leu Val Ser Pro Asn Ser Ser His Ser His Ala Val Val Leu Ser Trp

20 25 30

Val Arg Pro Phe Asp Gly Asn Ser Pro Ile Leu Tyr Tyr Ile Val Glu

35 40 45

Leu Ser Glu Asn Asn Ser Pro Trp Lys Val His Leu Ser Asn Val Gly

50 55 60

Pro Glu Met Thr Gly Val Thr Val Ser Gly Leu Thr Pro Ala Arg Thr

65 70 75 80

Tyr Gln Phe Arg Val Cys Ala Val Asn Glu Val Gly Arg Gly Gln Tyr

85

90

95

Ser Ala Glu Thr Ser Arg Leu Met Leu Pro Glu Glu Pro Pro Ser Ala

100

105

110

Pro Pro Lys Asn Ile Val Ala Ser Gly Arg Thr Asn Gln Ser Ile Met

115

120

125

Val Gln Trp Gln Pro Pro Pro Glu Thr Glu His Asn Gly Val Leu Arg

130

135

140

Gly Tyr Ile Leu Arg Tyr Arg Leu Ala Gly Leu Pro Gly Glu Tyr Gln

145

150

155

160

Gln Arg Asn Ile Thr Ser Pro Glu Val Asn Tyr Cys Leu Val Thr Asp

165

170

175

Leu Ile Ile Trp Thr Gln Tyr Glu Ile Gln Val Ala Ala Tyr Asn Gly

180

185

190

Ala Gly Leu Gly Val Phe Ser Arg Ala Val Thr Glu Tyr Thr Leu Gln

195

200

205

Gly Val Pro Thr Ala Pro Pro Gln Asn Val Gln Thr Glu Ala Val Asn

210

215

220

Ser Thr Thr Ile Gln Phe Leu Trp Asn Pro Pro Pro Gln Gln Phe Ile

225

230

235

240

$$\begin{aligned} & \text{all } \{U_{i,j}\}_{i,j \in \mathbb{N}} \text{ and } \{V_{i,j}\}_{i,j \in \mathbb{N}} \text{ are } \mathbb{N} \times \mathbb{N} \text{ matrices with } U_{i,j} = U_{j,i} \text{ and } V_{i,j} = V_{j,i} \\ & \text{in } \mathbb{N} \times \mathbb{N} \text{, } \{U_{i,j}\}_{i,j \in \mathbb{N}} \text{ and } \{V_{i,j}\}_{i,j \in \mathbb{N}} \text{ are } \mathbb{N} \times \mathbb{N} \text{ matrices with } U_{i,j} = U_{j,i} \text{ and } V_{i,j} = V_{j,i} \end{aligned}$$

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100

100

100

100

100

100

100

100

100

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<222> (22)..(1515)

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Met Ala Arg Leu Glu Val Ile Glu Leu Pro

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cat tca cct cag aac ctc ctg gtc agc cct aat tct tcc cac agc cac 99

His Ser Pro Gln Asn Leu Leu Val Ser Pro Asn Ser Ser His Ser His

15 20 25

gcc gtg gtg ctc tct tgg gtc cgg ccc ttt gat gga aac agt cct att 147

Ala Val Val Leu Ser Trp Val Arg Pro Phe Asp Gly Asn Ser Pro Ile

30 35 40

ctt tat tac atc gtg gag ctg tct gaa aac aac tct cca tgg aag gtg 195

Leu Tyr Tyr Ile Val Glu Leu Ser Glu Asn Asn Ser Pro Trp Lys Val

45 50 55

cat ctg tca aac gtt ggc cct gag atg aca ggc gtc acc gtg agt ggc 243

His Leu Ser Asn Val Gly Pro Glu Met Thr Gly Val Thr Val Ser Gly

60 65 70

ctg act ccg gct cgt acc tat caa ttc cgg gtg tgc gcg gtg aat gaa 291

Leu Thr Pro Ala Arg Thr Tyr Gln Phe Arg Val Cys Ala Val Asn Glu

75 80 85 90

gtg ggc agg ggc cag tac agt gcc gag aca agc agg ttg atg cta cct 339

Val Gly Arg Gly Gln Tyr Ser Ala Glu Thr Ser Arg Leu Met Leu Pro

95

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105

gaa gaa cca ccc agt gct ccc ccg aaa aat ata gtg gcc agt ggg cgg 387

Glu Glu Pro Pro Ser Ala Pro Pro Lys Asn Ile Val Ala Ser Gly Arg

110

115

120

act aat cag tcc att atg gtc cag tgg cag cca ccc cca gaa aca gag 435

Thr Asn Gln Ser Ile Met Val Gln Trp Gln Pro Pro Pro Glu Thr Glu

125

130

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cac aac ggg gtg ttg cgt gga tac atc ctc agg tac cgc ctg gct ggc 483

His Asn Gly Val Leu Arg Gly Tyr Ile Leu Arg Tyr Arg Leu Ala Gly

140

145

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ctt ccc gga gag tac cag cag cgg aac atc acc agc ccg gag gtg aac 531

Leu Pro Gly Glu Tyr Gln Gln Arg Asn Ile Thr Ser Pro Glu Val Asn

155

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165

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tac tgc ctg gtg aca gac ctg atc atc tgg aca cag tat gag ata cag 579

Tyr Cys Leu Val Thr Asp Leu Ile Ile Trp Thr Gln Tyr Glu Ile Gln

175

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185

gtg gcg gcg tac aac ggg gcc ggt ctg ggc gtc ttc agc agg gca gtg 627

Val Ala Ala Tyr Asn Gly Ala Gly Leu Gly Val Phe Ser Arg Ala Val

190

195

200

acc gag tac acc ttg cag gga gtg ccc acc gcg ccc ccg cag aac gtg 675

Thr Glu Tyr Thr Leu Gln Gly Val Pro Thr Ala Pro Pro Gln Asn Val

205

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215

cag acg gaa gcc gtg aac tcc acc acc att cag ttc ctg tgg aac cct 723
Gln Thr Glu Ala Val Asn Ser Thr Thr Ile Gln Phe Leu Trp Asn Pro

220

225

230

ccg cct cag cag ttt atc aat ggc atc aac cag gga tac aag ctt ctg 771
Pro Pro Gln Gln Phe Ile Asn Gly Ile Asn Gln Gly Tyr Lys Leu Leu

235

240

245

250

gca tgg ccg gca gat gcc ccc gag gct gtc act gtg gtc act att gcc 819
Ala Trp Pro Ala Asp Ala Pro Glu Ala Val Thr Val Val Thr Ile Ala

255

260

265

cca gat ttc cac gga gtc cac cat gga cac ata acg aac ctg aag aag 867
Pro Asp Phe His Gly Val His His Gly His Ile Thr Asn Leu Lys Lys

270

275

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ttt acc gcc tac ttc act tcc gtt ctg tgc ttc acc acc cct ggg gac 915
Phe Thr Ala Tyr Phe Thr Ser Val Leu Cys Phe Thr Thr Pro Gly Asp

285

290

295

ggg cct ccc agc aca cct cag ctg gtc tgg act cag gaa gac aaa cca 963
Gly Pro Pro Ser Thr Pro Gln Leu Val Trp Thr Gln Glu Asp Lys Pro

300

305

310

gga gct gtg gga cat ctg agt ttc aca gag atc ttg gac aca tct etc 1011
Gly Ala Val Gly His Leu Ser Phe Thr Glu Ile Leu Asp Thr Ser Leu

315

320

325

330

aag gtc agc tgg cag gag ccc ctg gag aaa aat ggc atc att act ggc 1059

Lys Val Ser Trp Gln Glu Pro Leu Glu Lys Asn Gly Ile Ile Thr Gly

335

340

345

tat cag atc tct tgg gaa gtg tac ggc agg aac gac tct cgt ctc acg 1107

Tyr Gln Ile Ser Trp Glu Val Tyr Gly Arg Asn Asp Ser Arg Leu Thr

350

355

360

cac acc ctg aac agc acg atg cac gag tac aag atc caa ggc ctc tca 1155

His Thr Leu Asn Ser Thr Met His Glu Tyr Lys Ile Gln Gly Leu Ser

365

370

375

tct ctc acc acc tac acc atc gac gtg gcc gct gtg act gcc gtg ggc 1203

Ser Leu Thr Thr Tyr Thr Ile Asp Val Ala Ala Val Thr Ala Val Gly

380

385

390

act ggc ctg gtg act tca tcc acc att tct tct gga gtg ccc cca gac 1251

Thr Gly Leu Val Thr Ser Ser Thr Ile Ser Ser Gly Val Pro Pro Asp

395

400

405

410

ctt cct ggt gcc cca tcc aac ctg gtc att tcc aac atc agc cct cgc 1299

Leu Pro Gly Ala Pro Ser Asn Leu Val Ile Ser Asn Ile Ser Pro Arg

415

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425

tcc gcc acc ctt cag ttc cgg cca ggc tat gac ggg aaa acg tcc atc 1347

Ser Ala Thr Leu Gln Phe Arg Pro Gly Tyr Asp Gly Lys Thr Ser Ile

430

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tcc agg tgg att gtt gag ggg cag atg aga cct gaa ggt gtt gga tta 1395

Ser Arg Trp Ile Val Glu Gly Gln Met Arg Pro Glu Gly Val Gly Leu

445

450

455

cct gcc gag gtc aca cag cca agc cat gaa gcc gga ttg gag cct gca 1443

Pro Ala Glu Val Thr Gln Pro Ser His Glu Ala Gly Leu Glu Pro Ala

460

465

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aac ctc gga agt ctg tgg ctg ctc agc ctg gtg tat tgg tgt tac agc 1491

Asn Leu Gly Ser Leu Trp Leu Leu Ser Leu Val Tyr Trp Cys Tyr Ser

475

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485

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cag aaa ctt tgg gaa ttc tct tgt tagttgggta gttttactgt aattttctat 1545

Gln Lys Leu Trp Glu Phe Ser Cys

495

aaagaattca tatcatctgt taatggcgac agtttttggt tcttccttg aattttttat 1605

attctttctt tctctttttt gtttcttctt ctttgagtat tttgtaatct tactgggagg 1665

gctaaagcgt cttctatcat atcgaattgg gacaatgata gaagacaatc tttgttttgt 1725

cactctaaag aaattattgt aagatTTTTat catcaggtat gacatttaca ccattgatgt 1785

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85 90 95

100 105 110

115 120 125

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Gly Tyr Ile Leu Arg Tyr Arg Leu Ala Gly Leu Pro Gly Glu Tyr Gln
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Gln Arg Asn Ile Thr Ser Pro Glu Val Asn Tyr Cys Leu Val Thr Asp
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Leu Ile Ile Trp Thr Gln Tyr Glu Ile Gln Val Ala Ala Tyr Asn Gly
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Ala Gly Leu Gly Val Phe Ser Arg Ala Val Thr Glu Tyr Thr Leu Gln
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Gly Val Pro Thr Ala Pro Pro Gln Asn Val Gln Thr Glu Ala Val Asn
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Ser Thr Thr Ile Gln Phe Leu Trp Asn Pro Pro Pro Gln Gln Phe Ile
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Asn Gly Ile Asn Gln Gly Tyr Lys Leu Leu Ala Trp Pro Ala Asp Ala
245 250 255

Pro Glu Ala Val Thr Val Val Thr Ile Ala Pro Asp Phe His Gly Val
260 265 270

His His Gly His Ile Thr Asn Leu Lys Lys Phe Thr Ala Tyr Phe Thr
231/735

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Gln Leu Val Trp Thr Gln Glu Asp Lys Pro Gly Ala Val Gly His Leu

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Ser Phe Thr Glu Ile Leu Asp Thr Ser Leu Lys Val Ser Trp Gln Glu

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Pro Leu Glu Lys Asn Gly Ile Ile Thr Gly Tyr Gln Ile Ser Trp Glu

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Val Tyr Gly Arg Asn Asp Ser Arg Leu Thr His Thr Leu Asn Ser Thr

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Thr His Glu Tyr Lys Ile Gln Gly Leu Ser Ser Leu Thr Thr Tyr Thr

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Ile Asp Val Ala Ala Val Thr Ala Val Gly Thr Gly Leu Val Thr Ser

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Ser Thr Ile Ser Ser Gly Val Pro Pro Asp Leu Pro Gly Ala Pro Ser

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Asn Leu Val Ile Ser Asn Ile Ser Pro Arg Ser Ala Thr Leu Gln Phe

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Arg Pro Gly Tyr Asp Gly Lys Thr Ser Ile Ser Arg Trp Ile Val Glu
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Gly Gln Met Arg His Gln Gly Val Gly Leu Pro Ala Glu Val Thr Gln
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Pro Ser His Glu Ala Gly Leu Glu Pro Ala Asn Leu Gly Ser Leu Trp
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His Ser Pro Gln Asn Leu Leu Val Ser Pro Asn Ser Ser His Ser His

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Leu Tyr Tyr Ile Val Glu Leu Ser Glu Asn Asn Ser Pro Trp Lys Val

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all other amino acids are present in the protein

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Lys Ala Ala Asp Pro Arg Phe Arg Pro Arg Trp Lys Val Ile Leu Thr

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Phe Phe Val Gly Ala Ala Ile Leu Trp Leu Leu Cys Ser His Arg Pro

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Ala Pro Gly Arg Pro Pro Thr His Asn Ala His Asn Trp Arg Leu Gly

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Gln Ala Pro Ala Asn Trp Tyr Asn Asp Thr Tyr Pro Leu Ser Pro Pro

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Lys Gly Arg Gly Met Glu Leu Ser Asp Leu Ile Val Phe Asn Gly Lys

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Leu Tyr Ser Val Asp Asp Arg Thr Gly Val Val Tyr Gln Ile Glu Gly

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Ser Lys Ala Val Pro Trp Val Ile Leu Ser Asp Gly Asp Gly Thr Val

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Glu Lys Gly Phe Lys Ala Glu Trp Leu Ala Val Arg Glu Ile Val Arg

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Gln Trp Ile Gln Arg

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240/735

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acgctg atg ccc gtg cag ctg tct gag cac ccg gaa tgg aat gag tct 168

Met Pro Val Gln Leu Ser Glu His Pro Glu Trp Asn Glu Ser

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atg cac tcc ctc cgg atc agt gtg ggg ggc ctt cct gtg ctg gcg tcc 216

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 Thr Val Glu Lys Gly Phe Lys Ala Glu Trp Leu Ala Val Arg Glu Ile
 242/735

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35 40 45

Glu Asp Leu Lys Ser Ile Leu Ser Glu Ala Pro Gly Lys Cys Val Pro

50 55 60

Tyr Ala Val Ile Glu Gly Ala Val Arg Ser Val Lys Glu Thr Leu Asn

65 70 75 80

Ser Gln Phe Val Glu Asn Cys Lys Gly Val Ile Gln Arg Leu Thr Leu

85 90 95

Gln Glu His Lys Met Val Trp Asn Arg Thr Thr His Leu Trp Asn Asp

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105

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Cys Ser Lys Ile Ile His Gln Arg Thr Asn Thr Val Pro Phe Asp Leu

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Val Pro His Glu Asp Gly Val Asp Val Ala Val Arg Val Leu Lys Pro

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Leu Asp Ser Val Asp Leu Gly Leu Glu Thr Val Tyr Glu Lys Phe His

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Pro Ser Ile Gln Ser Phe Thr Asp Val Ile Gly His Tyr Ile Ser Gly

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Glu Arg Pro Lys Gly Ile Gln Glu Thr Glu Glu Met Leu Lys Val Gly

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Ala Thr Leu Thr Gly Val Gly Glu Leu Val Leu Asp Asn Asn Ser Val

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Arg Leu Gln Pro Pro Lys Gln Gly Met Gln Tyr Tyr Leu Ser Ser Gln

210

215

220

Asp Phe Asp Ser Leu Leu Gln Arg Gln Glu Ser Ser Val Arg Leu Trp

225

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235

240

Lys Val Leu Ala Leu Val Phe Gly Phe Ala Thr Cys Ala Thr Leu Phe

245

250

255

[illegible]

265

270

[illegible]

280

285

Table 1

| Variable | Mean | SD | Min | Max |
|---------------------|------|-----|-----|-----|
| Age | 67.8 | 9.0 | 45 | 85 |
| Gender | | | | |
| Male | 50.0 | | | |
| Female | 50.0 | | | |
| Marital status | | | | |
| Married | 50.0 | | | |
| Single | 50.0 | | | |
| Widowed | 50.0 | | | |
| Divorced | 50.0 | | | |
| Educational level | | | | |
| High school or less | 50.0 | | | |
| College | 50.0 | | | |
| Postgraduate | 50.0 | | | |
| Income | | | | |
| Less than \$10,000 | 50.0 | | | |
| \$10,000-\$20,000 | 50.0 | | | |
| More than \$20,000 | 50.0 | | | |
| Health status | | | | |
| Excellent | 50.0 | | | |
| Good | 50.0 | | | |
| Fair | 50.0 | | | |
| Poor | 50.0 | | | |
| Depression | | | | |
| No depression | 50.0 | | | |
| Depression | 50.0 | | | |

295

300

[illegible]

310

315

320

Table 1. Demographic characteristics of study population

| | N (%) |
|-------------------------|------------|
| Age group (years) | |
| <60 | 79 (8.3) |
| 60-69 | 100 (10.6) |
| 70-79 | 100 (10.6) |
| ≥80 | 100 (10.6) |
| Total | 279 (29.5) |
| Gender | |
| Male | 100 (10.6) |
| Female | 179 (18.9) |
| Total | 279 (29.5) |
| Ethnicity | |
| Chinese | 100 (10.6) |
| Malay | 100 (10.6) |
| Indian | 100 (10.6) |
| Others | 100 (10.6) |
| Total | 279 (29.5) |
| Marital status | |
| Single | 100 (10.6) |
| Married | 100 (10.6) |
| Widowed | 100 (10.6) |
| Divorced | 100 (10.6) |
| Total | 279 (29.5) |
| Education level | |
| Primary school or below | 100 (10.6) |
| Secondary school | 100 (10.6) |
| Tertiary school | 100 (10.6) |
| Total | 279 (29.5) |

330

335

Table 1

| Variable | Mean | SD | Min | Max |
|---------------------|------|-----|-----|-----|
| Age | 67.8 | 9.0 | 50 | 85 |
| Gender | | | | |
| Male | 50.0 | | | |
| Female | 50.0 | | | |
| Educational level | | | | |
| High school or less | 20.0 | | | |
| College | 30.0 | | | |
| Postgraduate | 50.0 | | | |
| Marital status | | | | |
| Single | 10.0 | | | |
| Married | 90.0 | | | |
| Health status | | | | |
| Poor | 10.0 | | | |
| Good | 90.0 | | | |
| Depression | | | | |
| No | 50.0 | | | |
| Yes | 50.0 | | | |
| Medication | | | | |
| None | 10.0 | | | |
| One | 30.0 | | | |
| Two or more | 60.0 | | | |

345

350

<213> Homo sapiens

<222> (103).. (1158)

246/735

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tatccttgge gccacagtcg gccaccgggg ctcgccgccg tc atg gag agc gga 114

Met Glu Ser Gly

1

ggg egg ccc tgc ctg tgc cag ttc atc etc ctg ggc acc acc tct gtg 162

Gly Arg Pro Ser Leu Cys Gln Phe Ile Leu Leu Gly Thr Thr Ser Val

5 10 15 20

gtc acc gcc gcc ctg tac tcc gtg tac egg cag aag gcc egg gtc tcc 210

Val Thr Ala Ala Leu Tyr Ser Val Tyr Arg Gln Lys Ala Arg Val Ser

25 30 35

caa gag etc aag gga gct aaa aaa gtt cat ttg ggt gaa gat tta aag 258

Gln Glu Leu Lys Gly Ala Lys Lys Val His Leu Gly Glu Asp Leu Lys

40 45 50

agt att ctt tca gaa gct cca gga aaa tgc gtg cct tat gct gtt ata 306

Ser Ile Leu Ser Glu Ala Pro Gly Lys Cys Val Pro Tyr Ala Val Ile

55 60 65

gaa gga gct gtg cgg tct gtt aaa gaa acg ctt aac agc cag ttt gtg 354

Glu Gly Ala Val Arg Ser Val Lys Glu Thr Leu Asn Ser Gln Phe Val

70 75 80

gaa aac tgc aag ggg gta att cag cgg ctg aca ctt cag gag cac aag 402

Glu Asn Cys Lys Gly Val Ile Gln Arg Leu Thr Leu Gln Glu His Lys

85 90 95 100

atg gtg tgg aat cga acc acc cac ctt tgg aat gat tgc tca aag atc 450

Met Val Trp Asn Arg Thr Thr His Leu Trp Asn Asp Cys Ser Lys Ile

105

110

115

att cat cag agg acc aac aca gtg ccc ttt gac ctg gtg ccc cac gag 498

Ile His Gln Arg Thr Asn Thr Val Pro Phe Asp Leu Val Pro His Glu

120

125

130

gat ggc gtg gat gtg gct gtg cga gtg ctg aag ccc ctg gac tca gtg 546

Asp Gly Val Asp Val Ala Val Arg Val Leu Lys Pro Leu Asp Ser Val

135

140

145

gat ctg ggt cta gag act gtg tat gag aag ttc cac ccc tcg att cag 594

Asp Leu Gly Leu Glu Thr Val Tyr Glu Lys Phe His Pro Ser Ile Gln

150

155

160

tcc ttc acc gat gtc atc ggc cac tac atc agc ggt gag cgg ccc aaa 642

Ser Phe Thr Asp Val Ile Gly His Tyr Ile Ser Gly Glu Arg Pro Lys

165

170

175

180

ggc atc caa gag acc gag gag atg ctg aag gtg ggg gcc acc ctc aca 690

Gly Ile Gln Glu Thr Glu Glu Met Leu Lys Val Gly Ala Thr Leu Thr

185

190

195

ggg gtt ggc gaa ctg gtc ctg gac aac aac tct gtc cgc ctg cag ccg 738

Gly Val Gly Glu Leu Val Leu Asp Asn Asn Ser Val Arg Leu Gln Pro

200

205

210

ccc aaa caa ggc atg cag tac tat cta agc agc cag gac ttc gac agc 786

Pro Lys Gln Gly Met Gln Tyr Tyr Leu Ser Ser Gln Asp Phe Asp Ser

215

220

225

ctg ctg cag agg cag gag tcg agc gtc agg ctc tgg aag gtg ctg gcg 834

Leu Leu Gln Arg Gln Glu Ser Ser Val Arg Leu Trp Lys Val Leu Ala

230

235

240

ctg gtt ttt ggc ttt gcc aca tgt gcc acc ctc ttc ttc att ctc cgg 882

Leu Val Phe Gly Phe Ala Thr Cys Ala Thr Leu Phe Phe Ile Leu Arg

245

250

255

260

aag cag tat ctg cag cgg cag gag cgc ctg cgc ctc aag cag atg cag 930

Lys Gln Tyr Leu Gln Arg Gln Glu Arg Leu Arg Leu Lys Gln Met Gln

265

270

275

gag gag ttc cag gag cat gag gcc cag ctg ctg agc cga gcc aag cct 978

Glu Glu Phe Gln Glu His Glu Ala Gln Leu Leu Ser Arg Ala Lys Pro

280

285

290

gag gac agg gag agt ctg aag agc gcc tgt gta gtg tgt ctg agc agc 1026

Glu Asp Arg Glu Ser Leu Lys Ser Ala Cys Val Val Cys Leu Ser Ser

295

300

305

ttc aag tcc tgc gtc ttt ctg gag tgt ggg cac gtt tgt tcc tgc acc 1074

Phe Lys Ser Cys Val Phe Leu Glu Cys Gly His Val Cys Ser Cys Thr

310

315

320

gag tgc tac cgc gcc ttg cca gag ccc aag aag tgc cct atc tgc aga 1122

[illegible]

345

350

tgaagtcagc acatccgctt ctgcccagat ggctcggggcc ccgggcaaca gattgaagag 1828

agatcatgtg aagggcagtt ggtcaggcag gcctcctggt ttcgccactg gccctgattt 1888

gaactcctgc cacttgggag agctcggggt ggtccctggt tttccctect ggagaatgag 1948

gcgcagagge ctcgcctect gaaggacgca gtgtggatgc cactggccta gtgtcctggc 2008

ctcacagctt ccttgcaagg ctgtcacaag gaaaagcagc cggctggcac cctgagcata 2068

tgccctcttg gggtccctc atccagcccg tcgcagcttt gacatcttgg tgtactcatg 2128

tcgcttctcc ttgtgttacc cctcccagt attaccattt gcccctcacc tgcccttggt 2188

gagcctttta gtgcaagaca gatggggctg ttttccccca cctctgagta gttggaggtc 2248

acatacacag ctcttttttt attgcccttt tctgcctctg aatgttccatc tctcgtctc 2308

ctttgtgcag gcgaggaagg ggtgccctca ggggccgaca ctagtgtgat gcagtgtcca 2368

gtgtgaacag cagaaattaa acatgttgca acc 2401

- <210> 75
- <211> 352
- <212> PRT
- <213> Homo sapiens

<400> 75

Met Glu Ser Gly Gly Arg Pro Ser Leu Cys Gln Phe Ile Leu Leu Gly

1 5 10 15

Thr Thr Ser Val Val Thr Ala Ala Leu Tyr Ser Val Tyr Arg Gln Lys
20 25 30

Ala Arg Val Ser Gln Glu Leu Lys Gly Ala Lys Lys Val His Leu Gly
35 40 45

Glu Asp Leu Lys Ser Ile Leu Ser Glu Ala Pro Gly Lys Cys Val Pro
50 55 60

Tyr Ala Val Ile Glu Gly Ala Val Arg Ser Val Lys Glu Thr Leu Asn
65 70 75 80

Ser Gln Phe Val Glu Asn Cys Lys Gly Val Ile Gln Arg Leu Thr Leu
85 90 95

Gln Glu His Lys Met Val Trp Asn Arg Thr Thr His Leu Trp Asn Asp
100 105 110

Cys Ser Lys Ile Ile His Gln Arg Thr Asn Thr Val Pro Phe Asp Leu
115 120 125

Val Pro His Glu Asp Gly Val Asp Val Ala Val Arg Val Leu Lys Pro
130 135 140

Leu Asp Ser Val Asp Leu Gly Leu Glu Thr Val Tyr Glu Lys Phe His
145 150 155 160

Pro Ser Ile Gln Ser Phe Thr Asp Val Ile Gly His Tyr Ile Ser Gly
252/735

165

170

175

Glu Arg Pro Lys Gly Ile Gln Glu Thr Glu Glu Met Leu Lys Val Gly

180

185

190

Ala Thr Leu Thr Gly Val Gly Glu Leu Val Leu Asp Asn Asn Ser Val

195

200

205

Arg Leu Gln Pro Pro Lys Gln Gly Met Gln Tyr Tyr Leu Ser Ser Gln

210

215

220

Asp Phe Asp Ser Leu Leu Gln Arg Gln Glu Ser Ser Val Arg Leu Trp

225

230

235

240

Lys Val Leu Ala Leu Val Phe Gly Phe Ala Thr Cys Ala Thr Leu Phe

245

250

255

Phe Ile Leu Arg Lys Gln Tyr Leu Gln Arg Gln Glu Arg Leu Arg Leu

260

265

270

Lys Gln Met Gln Glu Glu Phe Gln Glu His Glu Ala Gln Leu Leu Ser

275

280

285

Arg Ala Lys Pro Glu Asp Arg Glu Ser Leu Lys Ser Ala Cys Val Val

290

295

300

Cys Leu Ser Ser Phe Lys Ser Cys Val Phe Leu Glu Cys Gly His Val

305

310

315

320

Cys Ser Cys Thr Glu Cys Tyr Arg Ala Leu Pro Glu Pro Lys Lys Cys

325

330

335

Pro Ile Cys Arg Gln Ala Ile Thr Arg Val Ile Pro Leu Tyr Asn Ser

340

345

350

<210> 76

<211> 2401

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (103).. (1158)

<400> 76

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tatccttggc gccacagtcg gccaccgggg ctgcgcgcgc tc atg gag agc gga 114

Met Glu Ser Gly

1

ggg cgg ccc tcg ctg tgc cag ttc atc ctc ctg ggc acc acc tct gtg 162

Gly Arg Pro Ser Leu Cys Gln Phe Ile Leu Leu Gly Thr Thr Ser Val

5

10

15

20

gtc acc gcc gcc ctg tac tcc gtg tac cgg cag aag gcc cgg gtc tcc 210

Val Thr Ala Ala Leu Tyr Ser Val Tyr Arg Gln Lys Ala Arg Val Ser

254/735

... ..

25

30

35

caa gag ctc aag gga gct aaa aaa gtt cat ttg ggt gaa gat tta aag 258

Gln Glu Leu Lys Gly Ala Lys Lys Val His Leu Gly Glu Asp Leu Lys

40

45

50

agt att ctt tca gaa gct cca gga aaa tgc gtg cct tat gct gtt ata 306

Ser Ile Leu Ser Glu Ala Pro Gly Lys Cys Val Pro Tyr Ala Val Ile

55

60

65

gaa gga gct gtg cgg tct gtt aaa gaa acg ctt aac agc cag ttt gtg 354

Glu Gly Ala Val Arg Ser Val Lys Glu Thr Leu Asn Ser Gln Phe Val

70

75

80

gaa aac tgc aag ggg gta att cag cgg ctg aca ctt cag gag cac aag 402

Glu Asn Cys Lys Gly Val Ile Gln Arg Leu Thr Leu Gln Glu His Lys

85

90

95

100

atg gtg tgg aat cga acc acc cac ctt tgg aat gat tgc tca aag atc 450

Met Val Trp Asn Arg Thr Thr His Leu Trp Asn Asp Cys Ser Lys Ile

105

110

115

att cat cag agg acc aac aca gtg ccc ttt gac ctg gtg ccc cac gag 498

Ile His Gln Arg Thr Asn Thr Val Pro Phe Asp Leu Val Pro His Glu

120

125

130

gat ggc gtg gat gtg gct gtg cga gtg ctg aag ccc ctg gac tca gtg 546

Asp Gly Val Asp Val Ala Val Arg Val Leu Lys Pro Leu Asp Ser Val

135

140

145

255/735

gat ctg ggt cta gag act gtg tat gag aag ttc cac ccc tcg att cag 594

Asp Leu Gly Leu Glu Thr Val Tyr Glu Lys Phe His Pro Ser Ile Gln

150

155

160

tcc ttc acc gat gtc atc ggc cac tac atc agc ggt gag cgg ccc aaa 642

Ser Phe Thr Asp Val Ile Gly His Tyr Ile Ser Gly Glu Arg Pro Lys

165

170

175

180

ggc atc caa gag acc gag gag atg ctg aag gtg ggg gcc acc ctc aca 690

Gly Ile Gln Glu Thr Glu Glu Met Leu Lys Val Gly Ala Thr Leu Thr

185

190

195

ggg gtt ggc gaa ctg gtc ctg gac aac aac tct gtc cgc ctg cag ccg 738

Gly Val Gly Glu Leu Val Leu Asp Asn Asn Ser Val Arg Leu Gln Pro

200

205

210

ccc aaa caa ggc atg cag tac tat cta agc agc cag gac ttc gac agc 786

Pro Lys Gln Gly Met Gln Tyr Tyr Leu Ser Ser Gln Asp Phe Asp Ser

215

220

225

ctg ctg cag agg cag gag tcg agc gtc agg ctc tgg aag gtg ctg gcg 834

Leu Leu Gln Arg Gln Glu Ser Ser Val Arg Leu Trp Lys Val Leu Ala

230

235

240

ctg gtt ttt ggc ttt gcc aca tgt gcc acc ctc ttc ttc att ctc cgg 882

Leu Val Phe Gly Phe Ala Thr Cys Ala Thr Leu Phe Phe Ile Leu Arg

245

250

255

260

aag cag tat ctg cag cgg cag gag cgc ctg cgc ctc aag cag atg cag 930

Lys Gln Tyr Leu Gln Arg Gln Glu Arg Leu Arg Leu Lys Gln Met Gln

265

270

275

gag gag ttc cag gag cat gag gcc cag ctg ctg agc cga gcc aag cct 978

Glu Glu Phe Gln Glu His Glu Ala Gln Leu Leu Ser Arg Ala Lys Pro

280

285

290

gag gac agg gag agt ctg aag agc gcc tgt gta gtg tgt ctg agc agc 1026

Glu Asp Arg Glu Ser Leu Lys Ser Ala Cys Val Val Cys Leu Ser Ser

295

300

305

ttc aag tcc tgc gtc ttt ctg gag tgt ggg cac gtt tgt tcc tgc acc 1074

Phe Lys Ser Cys Val Phe Leu Glu Cys Gly His Val Cys Ser Cys Thr

310

315

320

gag tgc tac cgc gcc ttg cca gag ccc aag aag tgc cct atc tgc aga 1122

Glu Cys Tyr Arg Ala Leu Pro Glu Pro Lys Lys Cys Pro Ile Cys Arg

325

330

335

340

cag gcg atc acc cgg gtg ata ccc ctg tac aac agc taatagtttg 1168

Gln Ala Ile Thr Arg Val Ile Pro Leu Tyr Asn Ser

345

350

gaagccgcac agcttgacct ggaagcaccc ctgccccctt ttcagggatt tttatctcga 1228

ggcctttgga ggagcagtgg tgggggtagc tgtcacctcc aggtatgatt gagggaggaa 1288

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caaagccagt gatcagcage tcttctgttc ctgtgtcttc tgtttttttc tggatgaatcg 1528

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gaactcctgc cacttgggag agctcggggt ggteccctggt tttccctcct ggagaatgag 1948

gcgcagaggc ctgcctcct gaaggacgca gtgtggatgc cactggccta gtgtcctggc 2008

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gagcctttta gtgcaagaca gatggggctg ttttcccca cctctgagta gttggaggtc 2248

acatacacag ctcttttttt attgcccttt tctgcctctg aatgttcac tctcgtcctc 2308

ctttgtgcag gcgaggaagg ggtgccctca ggggccgaca ctagtgtgat gcagtgtcca 2368

gtgtgaacag cagaaattaa acatgttgca acc 2401

<210> 77

<211> 697

<212> PRT

<213> Homo sapiens

<400> 77

Met Cys Lys Ser Leu Arg Tyr Cys Phe Ser His Cys Leu Tyr Leu Ala

1 5 10 15

Met Thr Arg Leu Glu Glu Val Asn Arg Glu Val Asn Met His Ser Ser

20 25 30

Val Arg Tyr Leu Gly Tyr Leu Ala Arg Ile Asn Leu Leu Val Ala Ile

35 40 45

Cys Leu Gly Leu Tyr Val Arg Trp Glu Lys Thr Ala Asn Ser Leu Ile

50 55 60

Leu Val Ile Phe Ile Leu Gly Leu Phe Val Leu Gly Ile Ala Ser Ile

65 70 75 80

225 230 235 240

Ile Tyr Phe Ser Gly Leu Ser Val Thr Glu Arg Trp Lys Pro Phe Leu

245 250 255

Tyr Arg Gly Arg Ile Cys Arg Arg Leu Ser Val Val Phe Ala Gly Met

260 265 270

Ile Glu Leu Thr Phe Phe Ile Leu Ser Ala Phe Lys Leu Arg Asp Thr

275 280 285

His Leu Trp Tyr Phe Val Ile Pro Gly Phe Ser Ile Phe Gly Ile Phe

290 295 300

Trp Met Ile Cys His Ile Ile Phe Leu Leu Thr Leu Trp Gly Phe His

305 310 315 320

Thr Lys Leu Asn Asp Cys His Lys Val Tyr Phe Thr His Arg Thr Asp

325 330 335

Tyr Asn Ser Leu Asp Arg Ile Met Ala Ser Lys Gly Met Arg His Phe

340 345 350

Cys Leu Ile Ser Glu Gln Leu Val Phe Phe Ser Leu Leu Ala Thr Ala

355 360 365

Ile Leu Gly Ala Val Ser Trp Gln Pro Thr Asn Gly Ile Phe Leu Ser

370 375 380

Met Phe Leu Ile Val Leu Pro Leu Glu Ser Met Ala His Gly Leu Phe
385 390 395 400

His Glu Leu Gly Asn Cys Leu Gly Gly Thr Ser Val Gly Tyr Ala Ile
405 410 415

Val Ile Pro Thr Asn Phe Cys Ser Pro Asp Gly Gln Pro Thr Leu Leu
420 425 430

Pro Pro Glu His Val Gln Glu Leu Asn Leu Arg Ser Thr Gly Met Leu
435 440 445

Asn Ala Ile Gln Arg Phe Phe Ala Tyr His Met Ile Glu Thr Tyr Gly
450 455 460

Cys Asp Tyr Ser Thr Ser Gly Leu Ser Phe Asp Thr Leu His Ser Lys
465 470 475 480

Leu Lys Ala Phe Leu Glu Leu Arg Thr Val Asp Gly Pro Arg His Asp
485 490 495

Thr Tyr Ile Leu Tyr Tyr Ser Gly His Thr His Gly Thr Gly Glu Trp
500 505 510

Ala Leu Ala Gly Gly Asp Thr Leu Arg Leu Asp Thr Leu Ile Glu Trp
515 520 525

Trp Arg Glu Lys Asn Gly Ser Phe Cys Ser Arg Leu Ile Ile Val Leu
530 535 540

Asp Ser Glu Asn Ser Thr Pro Trp Val Lys Glu Val Arg Lys Ile Asn
545 550 555 560

Asp Gln Tyr Ile Ala Val Gln Gly Ala Glu Leu Ile Lys Thr Val Asp
565 570 575

Ile Glu Glu Ala Asp Pro Pro Gln Leu Gly Asp Phe Thr Lys Asp Trp
580 585 590

Val Glu Tyr Asn Cys Asn Ser Ser Asn Asn Ile Cys Trp Thr Glu Lys
595 600 605

Gly Arg Thr Val Lys Ala Val Tyr Gly Val Ser Lys Arg Trp Ser Asp
610 615 620

Tyr Thr Leu His Leu Pro Thr Gly Ser Asp Val Ala Lys His Trp Met
625 630 635 640

Leu His Phe Pro Arg Ile Thr Tyr Pro Leu Val His Leu Ala Asn Trp
645 650 655

Leu Cys Gly Leu Asn Leu Phe Trp Ile Cys Lys Thr Cys Phe Arg Cys
660 665 670

Leu Lys Arg Leu Lys Met Ser Trp Phe Leu Pro Thr Val Leu Asp Thr
675 680 685

Gly Gln Gly Phe Lys Leu Val Lys Ser
263/735

690

695

<210> 78

<211> 3008

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (372).. (2462)

<400> 78

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aaagtttacg ccgacactgg cctgtattag cgcgtatggc ctcgggccct cgttccccaa 120

ggcgtgccgc ctccctgttc tcagtcgcag gctgaagcct tgtctgctct cctccttttt 180

ggtttggttt tggaactgac tccgagggtt gggagagcgc gttggtggcg acggccgagt 240

cagatcacta taaacaaaat ttccacaaga gaaaatgttg aaataggagt tgcggataca 300

ttggatatac tggatgaaat acaagcggtt aatttttgta acgtgaggga aaagcccaca 360

ttgctggtta c atg tgt aaa tca ctg cgt tat tgc ttt agt cat tgt etc 410

Met Cys Lys Ser Leu Arg Tyr Cys Phe Ser His Cys Leu

1

5

10

tat tta gca atg aca aga ctg gaa gaa gta aat aga gaa gtg aac atg 458
Tyr Leu Ala Met Thr Arg Leu Glu Glu Val Asn Arg Glu Val Asn Met
15 20 25

cat tct tca gtg cgg tat ctt ggc tat tta gcc aga atc aat tta ttg 506
His Ser Ser Val Arg Tyr Leu Gly Tyr Leu Ala Arg Ile Asn Leu Leu
30 35 40 45

gtt gct ata tgc tta ggt cta tac gta aga tgg gaa aaa aca gca aat 554
Val Ala Ile Cys Leu Gly Leu Tyr Val Arg Trp Glu Lys Thr Ala Asn
50 55 60

tcc tta att ttg gta att ttt att ctt ggt ctt ttt gtt ctt gga atc 602
Ser Leu Ile Leu Val Ile Phe Ile Leu Gly Leu Phe Val Leu Gly Ile
65 70 75

gcc agc ata ctc tat tac tat ttt tca atg gaa gca gca agt tta agt 650
Ala Ser Ile Leu Tyr Tyr Tyr Phe Ser Met Glu Ala Ala Ser Leu Ser
80 85 90

ctc tcc aat ctt tgg ttt gga ttc ttg ctt ggc ctc cta tgt ttt ctt 698
Leu Ser Asn Leu Trp Phe Gly Phe Leu Leu Gly Leu Leu Cys Phe Leu
95 100 105

gat aat tca tcc ttt aaa aat gat gta aaa gaa gaa tca acc aaa tat 746
Asp Asn Ser Ser Phe Lys Asn Asp Val Lys Glu Glu Ser Thr Lys Tyr
110 115 120 125

ttg ctt cta aca tcc ata gtg tta agg ata ttg tgc tct ctg gtg gag 794

Leu Leu Leu Thr Ser Ile Val Leu Arg Ile Leu Cys Ser Leu Val Glu

130

135

140

aga att tct ggt tat gtc cgt cat cgg ccc act tta cta acc aca gtt 842

Arg Ile Ser Gly Tyr Val Arg His Arg Pro Thr Leu Leu Thr Thr Val

145

150

155

gaa ttt ctg gag ctt gtt gga ttt gcc att gcc agc aca act atg ttg 890

Glu Phe Leu Glu Leu Val Gly Phe Ala Ile Ala Ser Thr Thr Met Leu

160

165

170

gtg gag aag tct ctg agt gtc att ttg ctt gtt gta gct ctg gct atg 938

Val Glu Lys Ser Leu Ser Val Ile Leu Leu Val Val Ala Leu Ala Met

175

180

185

ctg att att gat ctg aga atg aaa tct ttc tta gct att cca aac tta 986

Leu Ile Ile Asp Leu Arg Met Lys Ser Phe Leu Ala Ile Pro Asn Leu

190

195

200

205

gtt att ttt gca gtt ttg tta ttt ttt tcc tca ttg gaa act ccc aaa 1034

Val Ile Phe Ala Val Leu Leu Phe Phe Ser Ser Leu Glu Thr Pro Lys

210

215

220

aat ccg att gct ttt gcg tgt ttt ttt att tgc ctg ata act gat cct 1082

Asn Pro Ile Ala Phe Ala Cys Phe Phe Ile Cys Leu Ile Thr Asp Pro

225

230

235

ttc ctt gac att tat ttt agt gga ctt tca gta act gaa aga tgg aaa 1130

Phe Leu Asp Ile Tyr Phe Ser Gly Leu Ser Val Thr Glu Arg Trp Lys

gca aca gcg att ttg gga gca gtt tcc tgg cag cca aca aat gga att 1514

Ala Thr Ala Ile Leu Gly Ala Val Ser Trp Gln Pro Thr Asn Gly Ile

370

375

380

ttc ttg agc atg ttt cta atc gtt ttg cca ttg gaa tcc atg gct cat 1562

Phe Leu Ser Met Phe Leu Ile Val Leu Pro Leu Glu Ser Met Ala His

385

390

395

ggg ctc ttc cat gaa ttg ggt aac tgt tta gga gga aca tct gtt gga 1610

Gly Leu Phe His Glu Leu Gly Asn Cys Leu Gly Gly Thr Ser Val Gly

400

405

410

tat gct att gtg att ccc acc aac ttc tgc agt cct gat ggt cag cca 1658

Tyr Ala Ile Val Ile Pro Thr Asn Phe Cys Ser Pro Asp Gly Gln Pro

415

420

425

aca ctg ctt ccc cca gaa cat gta cag gag tta aat ttg agg tct act 1706

Thr Leu Leu Pro Pro Glu His Val Gln Glu Leu Asn Leu Arg Ser Thr

430

435

440

445

ggc atg ctc aat gct atc caa aga ttt ttt gca tat cat atg att gag 1754

Gly Met Leu Asn Ala Ile Gln Arg Phe Phe Ala Tyr His Met Ile Glu

450

455

460

acc tat gga tgt gac tat tcc aca agt gga ctg tca ttt gat act ctg 1802

Thr Tyr Gly Cys Asp Tyr Ser Thr Ser Gly Leu Ser Phe Asp Thr Leu

465

470

475

cat tcc aaa cta aaa gct ttc ctc gaa ctt cgg aca gtg gat gga ccc 1850

His Ser Lys Leu Lys Ala Phe Leu Glu Leu Arg Thr Val Asp Gly Pro

480

485

490

aga cat gat acg tat att ttg tat tac agt ggg cac acc cat ggt aca 1898

Arg His Asp Thr Tyr Ile Leu Tyr Tyr Ser Gly His Thr His Gly Thr

495

500

505

gga gag tgg gct cta gca ggt gga gat aca cta cgc ctt gac aca ctt 1946

Gly Glu Trp Ala Leu Ala Gly Gly Asp Thr Leu Arg Leu Asp Thr Leu

510

515

520

525

ata gaa tgg tgg aga gaa aag aat ggt tcc ttt tgt tcc cgg ctt att 1994

Ile Glu Trp Trp Arg Glu Lys Asn Gly Ser Phe Cys Ser Arg Leu Ile

530

535

540

atc gta tta gac agc gaa aat tca acc cct tgg gtg aaa gaa gtg agg 2042

Ile Val Leu Asp Ser Glu Asn Ser Thr Pro Trp Val Lys Glu Val Arg

545

550

555

aaa att aat gac cag tat att gca gtg caa gga gca gag ttg ata aaa 2090

Lys Ile Asn Asp Gln Tyr Ile Ala Val Gln Gly Ala Glu Leu Ile Lys

560

565

570

aca gta gat att gaa gaa gct gac ccg cca cag cta ggt gac ttt aca 2138

Thr Val Asp Ile Glu Glu Ala Asp Pro Pro Gln Leu Gly Asp Phe Thr

575

580

585

aaa gac tgg gta gaa tat aac tgc aac tcc agt aat aac atc tgc tgg 2186

Lys Asp Trp Val Glu Tyr Asn Cys Asn Ser Ser Asn Asn Ile Cys Trp
 590 595 600 605

act gaa aag gga cgc aca gtg aaa gca gta tat ggt gtg tca aaa cgg 2234
 Thr Glu Lys Gly Arg Thr Val Lys Ala Val Tyr Gly Val Ser Lys Arg
 610 615 620

tgg agt gac tac act ctg cat ttg cca acg gga agc gat gtg gcc aag 2282
 Trp Ser Asp Tyr Thr Leu His Leu Pro Thr Gly Ser Asp Val Ala Lys
 625 630 635

cac tgg atg tta cac ttt cct cgt att aca tat ccc cta gtg cat ttg 2330
 His Trp Met Leu His Phe Pro Arg Ile Thr Tyr Pro Leu Val His Leu
 640 645 650

gca aat tgg tta tgc ggt ctg aac ctt ttt tgg atc tgc aaa act tgt 2378
 Ala Asn Trp Leu Cys Gly Leu Asn Leu Phe Trp Ile Cys Lys Thr Cys
 655 660 665

ttt agg tgc ttg aaa aga tta aaa atg agt tgg ttt ctt cct act gtg 2426
 Phe Arg Cys Leu Lys Arg Leu Lys Met Ser Trp Phe Leu Pro Thr Val
 670 675 680 685

ctg gac aca gga caa ggc ttc aaa ctt gtc aaa tct taatttgac 2472
 Leu Asp Thr Gly Gln Gly Phe Lys Leu Val Lys Ser
 690 695

cccaaagcgg gatattaata agcactcata ctaccaatta tcactaactt gccatttttt 2532

gtatgctgta tttttatttg tggaaaatac ctgctactt ctgtagctgc tctcactttg 2592

tcttttctta agtaattatg gtatatataa ggcgttggga aaaaacattt tataatgaaa 2652

gtatgtaggg agtcaaatgc ttactgtaaa tgcataagag acgttaaaaa taacactgca 2712

ctttcaggaa tgtttgctta tggctctgat tagaaagaaa cagttgtcta tgctctgcaa 2772

tggccaatga tgaattacta atgccttatt ttctagggcat ataataatag tttagagaat 2832

gtagaccaga taaatttggt tactgtttta agaaaactac cagtttactt acagaagatt 2892

cttttttcca aacagtaggt ttcaccaag accatttgaa gaactgcaaa ctctttctct 2952

tagaaaagaa agagggcagc ctaaaataaa cgcaaaattt gettatactc catcac 3008

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25

30

Lys Glu Glu Ser Thr Lys Tyr Leu Leu Leu Thr Ser Ile Val Leu Arg

35

40

45

Ile Leu Cys Ser Leu Val Glu Arg Ile Ser Gly Tyr Val Arg His Arg

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55

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Pro Thr Leu Leu Thr Thr Val Glu Phe Leu Glu Leu Val Gly Phe Ala

65

70

75

80

Ile Ala Ser Thr Thr Met Leu Val Glu Lys Ser Leu Ser Val Ile Leu

85

90

95

Leu Val Val Ala Leu Ala Met Leu Ile Ile Asp Leu Arg Met Lys Ser

100

105

110

Phe Leu Ala Ile Pro Asn Leu Val Ile Phe Ala Val Leu Leu Phe Phe

115

120

125

Ser Ser Leu Glu Thr Pro Lys Asn Pro Ile Ala Phe Ala Cys Phe Phe

130

135

140

Ile Cys Leu Ile Thr Asp Pro Phe Leu Asp Ile Tyr Phe Ser Gly Leu

145

150

155

160

Ser Val Thr Glu Arg Trp Lys Pro Phe Leu Tyr Arg Gly Arg Ile Cys

165

170

175

Arg Arg Leu Ser Val Val Phe Ala Gly Met Ile Glu Leu Thr Phe Phe

180

185

190

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Ile Leu Ser Ala Phe Lys Leu Arg Asp Thr His Leu Trp Tyr Phe Val
195 200 205

Ile Pro Gly Phe Ser Ile Phe Gly Ile Phe Trp Met Ile Cys His Ile
210 215 220

Ile Phe Leu Leu Thr Leu Trp Gly Phe His Thr Lys Leu Asn Asp Cys
225 230 235 240

His Lys Val Tyr Phe Thr His Arg Thr Asp Tyr Asn Ser Leu Asp Arg
245 250 255

Ile Met Ala Ser Lys Gly Met Arg His Phe Cys Leu Ile Ser Glu Gln
260 265 270

Leu Val Phe Phe Ser Leu Leu Ala Thr Ala Ile Leu Gly Ala Val Ser
275 280 285

Trp Gln Pro Thr Asn Gly Ile Phe Leu Ser Met Phe Leu Ile Val Leu
290 295 300

Pro Leu Glu Ser Met Ala His Gly Leu Phe His Glu Leu Gly Asn Cys
305 310 315 320

Leu Gly Gly Thr Ser Val Gly Tyr Ala Ile Val Ile Pro Thr Asn Phe
325 330 335

Cys Ser Pro Asp Gly Gln Pro Thr Leu Leu Pro Pro Glu His Val Gln
273/735

Pro Gln Leu Gly Asp Phe Thr Lys Asp Trp Val Glu Tyr Asn Cys Asn
500 505 510

Ser Ser Asn Asn Ile Cys Trp Thr Glu Lys Gly Arg Thr Val Lys Ala
515 520 525

Val Tyr Gly Val Ser Lys Arg Trp Ser Asp Tyr Thr Leu His Leu Pro
530 535 540

Thr Gly Ser Asp Val Ala Lys His Trp Met Leu His Phe Pro Arg Ile
545 550 555 560

Thr Tyr Pro Leu Val His Leu Ala Asn Trp Leu Cys Gly Leu Asn Leu
565 570 575

Phe Trp Ile Cys Lys Thr Cys Phe Arg Cys Leu Lys Arg Leu Lys Met
580 585 590

Ser Trp Phe Leu Pro Thr Val Leu Asp Thr Gly Gln Gly Phe Lys Leu
595 600 605

Val Lys Ser
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<213> Homo sapiens

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ggcgtgccgc ctccctgttc tcagtcgcag gctgaagcct tgtctgctct cctccttttt 180

ggtttggttt tggaactgac tccgagggtt gggagagcgc gttggtggcg acggccgagt 240

cagatcacta taaacaaaat ttccacaaga gaaaatgttg aaataggagt tgcggataca 300

ttggatatac tggatgaaat acaagcggtt aattttttgta acgtgaggga aaagcccaca 360

ttgctggtta catgtgtaaa tcaactgcgtt attgcttttag tcattgtctc tatttagcaa 420

tgacaagact ggaagaagta aatagagaag tgaacatgca ttcttcagtg cggtatcttg 480

ctatttagcc agaatcaatt tattggttgc tatatgctta ggtctatacg taagatggga 540

aaaaacagca aattccttaa ttttggtaat ttttattctt ggtctttttg ttcttggaat 600

cgccagcata ctctattact atttttca atg gaa gca gca agt tta agt etc 652

Met Glu Ala Ala Ser Leu Ser Leu

tcc aat ctt tgg ttt gga ttc ttg ctt ggc ctc cta tgt ttt ctt gat 700

Ser Asn Leu Trp Phe Gly Phe Leu Leu Gly Leu Leu Cys Phe Leu Asp

10

15

20

aat tca tcc ttt aaa aat gat gta aaa gaa gaa tca acc aaa tat ttg 748

Asn Ser Ser Phe Lys Asn Asp Val Lys Glu Glu Ser Thr Lys Tyr Leu

25

30

35

40

ctt cta aca tcc ata gtg tta agg ata ttg tgc tct ctg gtg gag aga 796

Leu Leu Thr Ser Ile Val Leu Arg Ile Leu Cys Ser Leu Val Glu Arg

45

50

55

att tct ggt tat gtc cgt cat cgg ccc act tta cta acc aca gtt gaa 844

Ile Ser Gly Tyr Val Arg His Arg Pro Thr Leu Leu Thr Thr Val Glu

60

65

70

ttt ctg gag ctt gtt gga ttt gcc att gcc agc aca act atg ttg gtg 892

Phe Leu Glu Leu Val Gly Phe Ala Ile Ala Ser Thr Thr Met Leu Val

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85

gag aag tct ctg agt gtc att ttg ctt gtt gta gct ctg gct atg ctg 940

Glu Lys Ser Leu Ser Val Ile Leu Leu Val Val Ala Leu Ala Met Leu

90

95

100

att att gat ctg aga atg aaa tct ttc tta gct att cca aac tta gtt 988

Ile Ile Asp Leu Arg Met Lys Ser Phe Leu Ala Ile Pro Asn Leu Val

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115

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att ttt gca gtt ttg tta ttt ttt tcc tca ttg gaa act ccc aaa aat 1036

Ile Phe Ala Val Leu Leu Phe Phe Ser Ser Leu Glu Thr Pro Lys Asn

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130

135

ccg att gct ttt gcg tgt ttt ttt att tgc ctg ata act gat cct ttc 1084

Pro Ile Ala Phe Ala Cys Phe Phe Ile Cys Leu Ile Thr Asp Pro Phe

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ctt gac att tat ttt agt gga ctt tca gta act gaa aga tgg aaa ccc 1132

Leu Asp Ile Tyr Phe Ser Gly Leu Ser Val Thr Glu Arg Trp Lys Pro

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ttt ttg tac cgt gga aga att tgc aga aga ctt tca gtc gtt ttt gct 1180

Phe Leu Tyr Arg Gly Arg Ile Cys Arg Arg Leu Ser Val Val Phe Ala

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gga atg att gag ctt aca ttt ttt att ctt tcc gca ttc aaa ctt aga 1228

Gly Met Ile Glu Leu Thr Phe Phe Ile Leu Ser Ala Phe Lys Leu Arg

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190

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gac act cac ctc tgg tat ttt gta ata cct ggc ttt tcc att ttt gga 1276

Asp Thr His Leu Trp Tyr Phe Val Ile Pro Gly Phe Ser Ile Phe Gly

205

210

215

att ttc tgg atg att tgt cat att att ttt ctt tta act ctt tgg gga 1324

Ile Phe Trp Met Ile Cys His Ile Ile Phe Leu Leu Thr Leu Trp Gly

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225

230

ttc cat acc aaa tta aat gac tgc cat aaa gta tat ttt act cac agg 1372

Phe His Thr Lys Leu Asn Asp Cys His Lys Val Tyr Phe Thr His Arg

235

240

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aca gat tac aat agc ctt gat aga atc atg gca tcc aaa ggg atg cgc 1420

Thr Asp Tyr Asn Ser Leu Asp Arg Ile Met Ala Ser Lys Gly Met Arg

250

255

260

cat ttt tgc ttg att tca gag cag ttg gtg ttc ttt agt ctt ctt gca 1468

His Phe Cys Leu Ile Ser Glu Gln Leu Val Phe Phe Ser Leu Leu Ala

265

270

275

280

aca gcg att ttg gga gca gtt tcc tgg cag cca aca aat gga att ttc 1516

Thr Ala Ile Leu Gly Ala Val Ser Trp Gln Pro Thr Asn Gly Ile Phe

285

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ttg agc atg ttt cta atc gtt ttg cca ttg gaa tcc atg gct cat ggg 1564

Leu Ser Met Phe Leu Ile Val Leu Pro Leu Glu Ser Met Ala His Gly

300

305

310

ctc ttc cat gaa ttg ggt aac tgt tta gga gga aca tct gtt gga tat 1612

Leu Phe His Glu Leu Gly Asn Cys Leu Gly Gly Thr Ser Val Gly Tyr

315

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gct att gtg att ccc acc aac ttc tgc agt cct gat ggt cag cca aca 1660

Ala Ile Val Ile Pro Thr Asn Phe Cys Ser Pro Asp Gly Gln Pro Thr

330

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340

ctg ctt ccc cca gaa cat gta cag gag tta aat ttg agg tct act ggc 1708

Leu Leu Pro Pro Glu His Val Gln Glu Leu Asn Leu Arg Ser Thr Gly

345 350 355 360

atg ctc aat gct atc caa aga ttt ttt gca tat cat atg att gag acc 1756
Met Leu Asn Ala Ile Gln Arg Phe Phe Ala Tyr His Met Ile Glu Thr

365 370 375

tat gga tgt gac tat tcc aca agt gga ctg tca ttt gat act ctg cat 1804
Tyr Gly Cys Asp Tyr Ser Thr Ser Gly Leu Ser Phe Asp Thr Leu His

380 385 390

tcc aaa cta aaa gct ttc ctc gaa ctt cgg aca gtg gat gga ccc aga 1852
Ser Lys Leu Lys Ala Phe Leu Glu Leu Arg Thr Val Asp Gly Pro Arg

395 400 405

cat gat acg tat att ttg tat tac agt ggg cac acc cat ggt aca gga 1900
His Asp Thr Tyr Ile Leu Tyr Tyr Ser Gly His Thr His Gly Thr Gly

410 415 420

gag tgg gct cta gca ggt gga gat aca cta cgc ctt gac aca ctt ata 1948
Glu Trp Ala Leu Ala Gly Gly Asp Thr Leu Arg Leu Asp Thr Leu Ile

425 430 435 440

gaa tgg tgg aga gaa aag aat ggt tcc ttt tgt tcc cgg ctt att atc 1996
Glu Trp Trp Arg Glu Lys Asn Gly Ser Phe Cys Ser Arg Leu Ile Ile

445 450 455

gta tta gac agc gaa aat tca acc cct tgg gtg aaa gaa gtg agg aaa 2044
Val Leu Asp Ser Glu Asn Ser Thr Pro Trp Val Lys Glu Val Arg Lys

460 465 470

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Ile Asn Asp Gln Tyr Ile Ala Val Gln Gly Ala Glu Leu Ile Lys Thr

475

480

485

gta gat att gaa gaa gct gac ccg cca cag cta ggt gac ttt aca aaa 2140

Val Asp Ile Glu Glu Ala Asp Pro Pro Gln Leu Gly Asp Phe Thr Lys

490

495

500

gac tgg gta gaa tat aac tgc aac tcc agt aat aac atc tgc tgg act 2188

Asp Trp Val Glu Tyr Asn Cys Asn Ser Ser Asn Asn Ile Cys Trp Thr

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510

515

520

gaa aag gga cgc aca gtg aaa gca gta tat ggt gtg tca aaa cgg tgg 2236

Glu Lys Gly Arg Thr Val Lys Ala Val Tyr Gly Val Ser Lys Arg Trp

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agt gac tac act ctg cat ttg cca acg gga agc gat gtg gcc aag cac 2284

Ser Asp Tyr Thr Leu His Leu Pro Thr Gly Ser Asp Val Ala Lys His

540

545

550

tgg atg tta cac ttt cct cgt att aca tat ccc cta gtg cat ttg gca 2332

Trp Met Leu His Phe Pro Arg Ile Thr Tyr Pro Leu Val His Leu Ala

555

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aat tgg tta tgc ggt ctg aac ctt ttt tgg atc tgc aaa act tgt ttt 2380

Asn Trp Leu Cys Gly Leu Asn Leu Phe Trp Ile Cys Lys Thr Cys Phe

570

575

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agg tgc ttg aaa aga tta aaa atg agt tgg ttt ctt cct act gtg ctg 2428

Arg Cys Leu Lys Arg Leu Lys Met Ser Trp Phe Leu Pro Thr Val Leu

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gac aca gga caa ggc ttc aaa ctt gtc aaa tct taatttggac cccaaagcgg 2481

Asp Thr Gly Gln Gly Phe Lys Leu Val Lys Ser

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<212> PRT

<213> Homo sapiens

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Gln Met Thr Val Tyr His Pro Gly Gln Leu Gln Cys Gly Ile Phe Gln

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Ser Ile Ser Phe Asn Arg Glu Lys Leu Pro Ser Ser Glu Val Val Lys

35 40 45

Phe Gly Arg Asn Ser Asn Ile Cys His Tyr Thr Phe Gln Asp Lys Gln

50 55 60

Val Ser Arg Val Gln Phe Ser Leu Gln Leu Phe Lys Lys Phe Asn Ser

65 70 75 80

Ser Val Leu Ser Phe Glu Ile Lys Asn Met Ser Lys Lys Thr Asn Leu

85 90 95

Ile Val Asp Ser Arg Glu Leu Gly Tyr Leu Asn Lys Met Asp Leu Pro

100 105 110

Tyr Arg Cys Met Val Arg Phe Gly Glu Tyr Gln Phe Leu Met Glu Lys

115 120 125

Glu Asp Gly Glu Ser Leu Glu Phe Phe Glu Thr Gln Phe Ile Leu Ser

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agagttcact gactccccag ccccaggtgg gccttgtgca cate atg acc agt ttt 296

Met Thr Ser Phe

1

gaa gat gct gac aca gaa gag aca gta act tgt ctc cag atg acg gtt 344

Glu Asp Ala Asp Thr Glu Glu Thr Val Thr Cys Leu Gln Met Thr Val

5 10 15 20

tac cat cct ggc cag ttg cag tgt gga ata ttt cag tca ata agt ttt 392

Tyr His Pro Gly Gln Leu Gln Cys Gly Ile Phe Gln Ser Ile Ser Phe

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aac aga gag aaa ctc cct tcc agc gaa gtg gtg aaa ttt ggc cga aat 440

Asn Arg Glu Lys Leu Pro Ser Ser Glu Val Val Lys Phe Gly Arg Asn

40 45 50

tcc aac atc tgt cat tat act ttt cag gac aaa cag gtt tcc cga gtt 488

Ser Asn Ile Cys His Tyr Thr Phe Gln Asp Lys Gln Val Ser Arg Val

55 60 65

cag ttt tct ctg cag ctg ttt aaa aaa ttc aac agc tca gtt ctc tcc 536

Gln Phe Ser Leu Gln Leu Phe Lys Lys Phe Asn Ser Ser Val Leu Ser

70 75 80

ttt gaa ata aaa aat atg agt aaa aag acc aat ctg atc gtg gac agc 584

Phe Glu Ile Lys Asn Met Ser Lys Lys Thr Asn Leu Ile Val Asp Ser

85 90 95 100

aga gag ctg ggc tac cta aat aaa atg gac ctg cca tac agg tgc atg 632

Arg Glu Leu Gly Tyr Leu Asn Lys Met Asp Leu Pro Tyr Arg Cys Met

105

110

115

gtc aga ttc gga gag tat cag ttt ctg atg gag aag gaa gat ggc gag 680

Val Arg Phe Gly Glu Tyr Gln Phe Leu Met Glu Lys Glu Asp Gly Glu

120

125

130

tca ttg gaa ttt ttt gag act caa ttt att tta tct cca aga tca etc 728

Ser Leu Glu Phe Phe Glu Thr Gln Phe Ile Leu Ser Pro Arg Ser Leu

135

140

145

ttg caa gaa aac aac tgg cca cca cac agg ccc ata ccg gag tat ggc 776

Leu Gln Glu Asn Asn Trp Pro Pro His Arg Pro Ile Pro Glu Tyr Gly

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155

160

act tat tcg etc tgc tcc tcc caa agc agt tct ccg aca gaa atg gat 824

Thr Tyr Ser Leu Cys Ser Ser Gln Ser Ser Ser Pro Thr Glu Met Asp

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170

175

180

gaa aat gag tca tgaacacaga aagtctaaga ggagaaatat gatggatgaa 876

Glu Asn Glu Ser

gagctctgta gatgctgtat agacactaaa taagagttga ttagggtagt atattatagt 936

catctgttat gctgtgaaat ttggaattca gtattatcat ttigaagtct gtaaattgtg 996

ttagtcatta acttagtcac ctgttgtatt ctggatctac acaaaattat tttaactgct 1056



20 25 30

35 40 45

50 55 60

65 70 75 80

85 90 95

100 105 110

115 120 125

130 135 140

145 150 155 160

288/735

11-11-68 11:11 AM 11-11-68 11:11 AM 11-11-68 11:11 AM 11-11-68 11:11 AM

165

170

175

Pro Arg His Gly Ala Pro Met Tyr Arg Tyr Ser Phe Ala Ser Leu Ser

180

185

190

Asn Val Leu Ser Ser Trp Cys Gln Tyr Glu Ala Leu Lys Phe Val Ser

195

200

205

Phe Pro Thr Gln Val Leu Ala Lys Ala Ser Lys Val Ile Pro Val Met

210

215

220

Leu Met Gly Lys Leu Val Ser Arg Arg Ser Tyr Glu His Trp Glu Tyr

225

230

235

240

Leu Thr Ala Thr Leu Ile Ser Ile Gly Val Ser Met Phe Leu Leu Ser

245

250

255

Ser Gly Pro Glu Pro Arg Ser Ser Pro Ala Thr Thr Leu Ser Gly Leu

260

265

270

Phe Thr Val Gly Ser Leu Leu Glu Gln Gly Ala Leu Leu Glu Gly Thr

275

280

285

Arg Phe Met Gly Arg His Ser Glu Phe Ala Ala His Ala Leu Leu Leu

290

295

300

Ser Ile Cys Ser Ala Cys Gly Gln Leu Phe Ile Phe Tyr Thr Ile Gly

305

310

315

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Gln Phe Gly Ala Ala Val Phe Thr Ile Ile Met Thr Leu Arg Gln Ala

325 330 335

Phe Ala Ile Leu Leu Ser Cys Leu Leu Tyr Gly His Thr Val Thr Val

340 345 350

Val Gly Gly Leu Gly Val Ala Val Val Phe Ala Ala Leu Leu Leu Arg

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Val Tyr Ala Arg Gly Arg Leu Lys Gln Arg Gly Lys Lys Ala Val Pro

370 375 380

Val Glu Ser Pro Val Gln Lys Val

385 390

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<213> Homo sapiens

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<400> 84

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cgcgcgggccc ggggactcgc attccccggt tccccctcca ccccacgcgg cctggacc 118

atg gac gcc aga tgg tgg gca gtg gtg gtg ctg gct gcg ttc ccc tcc 166

Met Asp Ala Arg Trp Trp Ala Val Val Val Leu Ala Ala Phe Pro Ser

1

5

10

15

cta ggg gca ggt ggg gag act ccc gaa gcc cct ccg gag tca tgg acc 214

Leu Gly Ala Gly Gly Glu Thr Pro Glu Ala Pro Pro Glu Ser Trp Thr

20

25

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cag cta tgg ttc ttc cga ttt gtg gtg aat gct gct ggc tat gcc agc 262

Gln Leu Trp Phe Phe Arg Phe Val Val Asn Ala Ala Gly Tyr Ala Ser

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ttt atg gta cct ggc tac ctc ctg gtg cag tac ttc agg cgg aag aac 310

Phe Met Val Pro Gly Tyr Leu Leu Val Gln Tyr Phe Arg Arg Lys Asn

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55

60

tac ctg gag acc ggt agg ggc ctc tgc ttt ccc ctg gtg aaa gct tgt 358

Tyr Leu Glu Thr Gly Arg Gly Leu Cys Phe Pro Leu Val Lys Ala Cys

65

70

75

80

gtg ttt ggc aat gag ccc aag gcc tct gat gag gtt ccc ctg gcg ccc 406

Val Phe Gly Asn Glu Pro Lys Ala Ser Asp Glu Val Pro Leu Ala Pro

85

90

95

cga aca gag gcg gca gag acc acc ccg atg tgg cag gcc ctg aag ctg 454

Arg Thr Glu Ala Ala Glu Thr Thr Pro Met Trp Gln Ala Leu Lys Leu

100

105

110

ctc ttc tgt gcc aca ggg ctc cag gtg tct tat ctg act tgg ggt gtg 502

Leu Phe Cys Ala Thr Gly Leu Gln Val Ser Tyr Leu Thr Trp Gly Val

115

120

125

ctg cag gaa aga gtg atg acc cgc agc tat ggg gcc aca gcc aca tca 550

Leu Gln Glu Arg Val Met Thr Arg Ser Tyr Gly Ala Thr Ala Thr Ser

130

135

140

ccg ggt gag cgc ttt acg gac tgc cag ttc ctg gtg cta atg aac cga 598

Pro Gly Glu Arg Phe Thr Asp Ser Gln Phe Leu Val Leu Met Asn Arg

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155

160

gtg ctg gca ctg att gtg gct ggc ctc tcc tgt gtt ctc tgc aag cag 646

Val Leu Ala Leu Ile Val Ala Gly Leu Ser Cys Val Leu Cys Lys Gln

165

170

175

ccc cgg cat ggg gca ccc atg tac cgg tac tcc ttt gcc agc ctg tcc 694

Pro Arg His Gly Ala Pro Met Tyr Arg Tyr Ser Phe Ala Ser Leu Ser

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185

190

aat gtg ctt agc agc tgg tgc caa tac gaa gct ctt aag ttc gtc agc 742

Asn Val Leu Ser Ser Trp Cys Gln Tyr Glu Ala Leu Lys Phe Val Ser

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200

205

ttc ccc acc cag gtg ctg gcc aag gcc tct aag gtg atc cct gtc atg 790

Phe Pro Thr Gln Val Leu Ala Lys Ala Ser Lys Val Ile Pro Val Met

210

215

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ctg atg gga aag ctt gtg tct cgg cgc agc tac gaa cac tgg gag tac 838

Leu Met Gly Lys Leu Val Ser Arg Arg Ser Tyr Glu His Trp Glu Tyr

225 230 235 240

ctg aca gcc acc ctc atc tcc att ggg gtc agc atg ttt ctg cta tcc 886

Leu Thr Ala Thr Leu Ile Ser Ile Gly Val Ser Met Phe Leu Leu Ser

245 250 255

agc gga cca gag ccc cgc agc tcc cca gcc acc aca ctc tca ggc ctc 934

Ser Gly Pro Glu Pro Arg Ser Ser Pro Ala Thr Thr Leu Ser Gly Leu

260 265 270

ttc aca gtg ggc tca ctg cta gaa cag ggg gcc cta ctg gag gga acc 982

Phe Thr Val Gly Ser Leu Leu Glu Gln Gly Ala Leu Leu Glu Gly Thr

275 280 285

cgc ttc atg ggg cga cac agt gag ttt gct gcc cat gcc ctg cta ctc 1030

Arg Phe Met Gly Arg His Ser Glu Phe Ala Ala His Ala Leu Leu Leu

290 295 300

tcc atc tgc tcc gca tgt ggc cag ctc ttc atc ttt tac acc att ggg 1078

Ser Ile Cys Ser Ala Cys Gly Gln Leu Phe Ile Phe Tyr Thr Ile Gly

305 310 315 320

cag ttt ggg gct gcc gtc ttc acc atc atc atg acc ctc cgc cag gcc 1126

Gln Phe Gly Ala Ala Val Phe Thr Ile Ile Met Thr Leu Arg Gln Ala

325 330 335

ttt gcc atc ctt ctt tcc tgc ctt ctc tat ggc cac act gtc act gtg 1174

Phe Ala Ile Leu Leu Ser Cys Leu Leu Tyr Gly His Thr Val Thr Val

340

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gtc tac gcg cgg ggc cgt cta aag caa cgg gga aag aag gct gtg cct 1270
Val Tyr Ala Arg Gly Arg Leu Lys Gln Arg Gly Lys Lys Ala Val Pro

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gtt gag tct cct gtg cag aag gtt tgagggtgga aagggcctga ggggtgaagt 1324
Val Glu Ser Pro Val Gln Lys Val

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ctgaggaaaag gggatgcaga gccctgcccc gcaccaccac ctccatgct cctggatccc 1804

Arg Thr Glu Ala Ala Glu Thr Thr Pro Met Trp Gln Ala Leu Lys Leu
 100 105 110

Leu Phe Cys Ala Thr Gly Leu Gln Val Ser Tyr Leu Thr Trp Gly Val
 115 120 125

Leu Gln Glu Arg Val Met Thr Arg Ser Tyr Gly Ala Thr Ala Thr Ser
 130 135 140

Pro Gly Glu Arg Phe Thr Asp Ser Gln Phe Leu Val Leu Met Asn Arg
 145 150 155 160

Val Leu Ala Leu Ile Val Ala Gly Leu Ser Cys Val Leu Cys Lys Gln
 165 170 175

Pro Arg His Gly Ala Pro Met Tyr Arg Tyr Ser Phe Ala Ser Leu Ser
 180 185 190

Asn Val Leu Ser Ser Trp Cys Gln Tyr Glu Ala Leu Lys Phe Val Ser
 195 200 205

Phe Pro Thr Gln Val Leu Ala Lys Ala Ser Lys Val Ile Pro Val Met
 210 215 220

Leu Met Gly Lys Leu Val Ser Arg Arg Ser Tyr Glu His Trp Glu Tyr
 225 230 235 240

Leu Thr Ala Thr Leu Ile Ser Ile Gly Val Ser Met Phe Leu Leu Ser
 296/735

245

250

255

Ser Gly Pro Glu Pro Arg Ser Ser Pro Ala Thr Thr Leu Ser Gly Leu

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Ile Leu Leu Ala Gly Tyr Ile Ala Phe Asp Ser Phe Thr Ser Asn Trp

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Gln Asp Ala Leu Phe Ala Tyr Lys Met Ser Ser Val Gln Met Met Phe

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300

Gly Val Asn Phe Phe Ser Cys Leu Phe Thr Val Gly Ser Leu Leu Glu

305

310

315

320

Gln Gly Ala Leu Leu Glu Gly Thr Arg Phe Met Gly Arg His Ser Glu

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330

335

Phe Ala Ala His Ala Leu Leu Leu Ser Ile Cys Ser Ala Cys Gly Gln

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Leu Phe Ile Phe Tyr Thr Ile Gly Gln Phe Gly Ala Ala Val Phe Thr

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365

Ile Ile Met Thr Leu Arg Gln Ala Phe Ala Ile Leu Leu Ser Cys Leu

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Leu Tyr Gly His Thr Val Thr Val Val Gly Gly Leu Gly Val Ala Val

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atg gac gcc aga tgg tgg gca gtg gtg gtg ctg gct gcg ttc ccc tcc 166

Met Asp Ala Arg Trp Trp Ala Val Val Val Leu Ala Ala Phe Pro Ser

1 5 10 15

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Leu Gly Ala Gly Gly Glu Thr Pro Glu Ala Pro Pro Glu Ser Trp Thr

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Gln Leu Trp Phe Phe Arg Phe Val Val Asn Ala Ala Gly Tyr Ala Ser

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ttt atg gta cct ggc tac ctc ctg gtg cag tac ttc agg cgg aag aac 310

Phe Met Val Pro Gly Tyr Leu Leu Val Gln Tyr Phe Arg Arg Lys Asn

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tac ctg gag acc ggt agg ggc ctc tgc ttt ccc ctg gtg aaa gct tgt 358

Tyr Leu Glu Thr Gly Arg Gly Leu Cys Phe Pro Leu Val Lys Ala Cys

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gtg ttt ggc aat gag ccc aag gcc tct gat gag gtt ccc ctg gcg ccc 406

Val Phe Gly Asn Glu Pro Lys Ala Ser Asp Glu Val Pro Leu Ala Pro

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cga aca gag gcg gca gag acc acc ccg atg tgg cag gcc ctg aag ctg 454

Arg Thr Glu Ala Ala Glu Thr Thr Pro Met Trp Gln Ala Leu Lys Leu

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ctc ttc tgt gcc aca ggg ctc cag gtg tct tat ctg act tgg ggt gtg 502

Leu Phe Cys Ala Thr Gly Leu Gln Val Ser Tyr Leu Thr Trp Gly Val

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ctg cag gaa aga gtg atg acc cgc agc tat ggg gcc aca gcc aca tca 550

Leu Gln Glu Arg Val Met Thr Arg Ser Tyr Gly Ala Thr Ala Thr Ser

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Pro Gly Glu Arg Phe Thr Asp Ser Gln Phe Leu Val Leu Met Asn Arg
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 165 170 175

ccc cgg cat ggg gca ccc atg tac cgg tac tcc ttt gcc agc ctg tcc 694
 Pro Arg His Gly Ala Pro Met Tyr Arg Tyr Ser Phe Ala Ser Leu Ser
 180 185 190

aat gtg ctt agc agc tgg tgc caa tac gaa gct ctt aag ttc gtc agc 742
 Asn Val Leu Ser Ser Trp Cys Gln Tyr Glu Ala Leu Lys Phe Val Ser
 195 200 205

ttc ccc acc cag gtg ctg gcc aag gcc tct aag gtg atc cct gtc atg 790
 Phe Pro Thr Gln Val Leu Ala Lys Ala Ser Lys Val Ile Pro Val Met
 210 215 220

ctg atg gga aag ctt gtg tct cgg cgc agc tac gaa cac tgg gag tac 838
 Leu Met Gly Lys Leu Val Ser Arg Arg Ser Tyr Glu His Trp Glu Tyr
 225 230 235 240

ctg aca gcc acc ctc atc tcc att ggg gtc agc atg ttt ctg cta tcc 886
 Leu Thr Ala Thr Leu Ile Ser Ile Gly Val Ser Met Phe Leu Leu Ser
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agc gga cca gag ccc cgc agc tcc cca gcc acc aca ctc tca ggc ctc 934
 Ser Gly Pro Glu Pro Arg Ser Ser Pro Ala Thr Thr Leu Ser Gly Leu

260

265

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atc tta ctg gca ggt tat att gct ttt gac agc ttc acc tca aac tgg 982

Ile Leu Leu Ala Gly Tyr Ile Ala Phe Asp Ser Phe Thr Ser Asn Trp

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cag gat gcc ctg ttt gcc tat aag atg tca tcg gtg cag atg atg ttt 1030

Gln Asp Ala Leu Phe Ala Tyr Lys Met Ser Ser Val Gln Met Met Phe

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ggg gtc aat ttc ttc tcc tgc ctc ttc aca gtg ggc tca ctg cta gaa 1078

Gly Val Asn Phe Phe Ser Cys Leu Phe Thr Val Gly Ser Leu Leu Glu

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315

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cag ggg gcc cta ctg gag gga acc cgc ttc atg ggg cga cac agt gag 1126

Gln Gly Ala Leu Leu Glu Gly Thr Arg Phe Met Gly Arg His Ser Glu

325

330

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ttt gct gcc cat gcc ctg cta ctc tcc atc tgc tcc gca tgt ggc cag 1174

Phe Ala Ala His Ala Leu Leu Leu Ser Ile Cys Ser Ala Cys Gly Gln

340

345

350

ctc ttc atc ttt tac acc att ggg cag ttt ggg gct gcc gtc ttc acc 1222

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atc atc atg acc ctc cgc cag gcc ttt gcc atc ctt ctt tcc tgc ctt 1270

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ctc tat ggc cac act gtc act gtg gtg gga ggg ctg ggg gtg gct gtg 1318

Leu Tyr Gly His Thr Val Thr Val Val Gly Gly Leu Gly Val Ala Val

385 390 395 400

gtc ttt gct gcc ctc ctg ctc aga gtc tac gcg cgg ggc cgt cta aag 1366

Val Phe Ala Ala Leu Leu Arg Val Tyr Ala Arg Gly Arg Leu Lys

405 410 415

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Gln Arg Gly Lys Lys Ala Val Pro Val Glu Ser Pro Val Gln Lys Val

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ctgc 2018

- <210> 87
- <211> 235
- <212> PRT
- <213> Homo sapiens

<400> 87

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Trp Gly Lys Arg His Ser Val Asp Thr Ser Pro Gly Tyr His Glu Ser
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Asp Ser Lys Lys Ser Glu Asp Leu Ser Leu Cys Asn Val Ala Glu His
35 40 45

Ser Asn Thr Thr Glu Gly Pro Thr Gly Lys Gln Glu Gly Ala Gln Ser
50 55 60

Val Glu Glu Met Phe Glu Glu Glu Ala Glu Glu Glu Val Phe Leu Lys
65 70 75 80

Phe Val Ile Leu His Ala Glu Asp Asp Thr Asp Glu Ala Leu Arg Val
303/735

85

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95

Gln Asn Leu Leu Gln Asp Asp Phe Gly Ile Lys Pro Gly Ile Ile Phe

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105

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Ala Glu Met Pro Cys Gly Arg Gln His Leu Gln Asn Leu Asp Asp Ala

115

120

125

Val Asn Gly Ser Ala Trp Thr Ile Leu Leu Leu Thr Glu Asn Phe Leu

130

135

140

Arg Asp Thr Trp Cys Asn Phe Gln Phe Tyr Thr Ser Leu Met Asn Ser

145

150

155

160

Val Asn Arg Gln His Lys Tyr Asn Ser Val Ile Pro Met Arg Pro Leu

165

170

175

Asn Asn Pro Leu Pro Arg Glu Arg Thr Pro Phe Ala Leu Gln Thr Ile

180

185

190

Asn Ala Leu Glu Glu Glu Ser Arg Gly Phe Pro Thr Gln Val Glu Arg

195

200

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Ile Phe Gln Glu Ser Val Tyr Lys Thr Gln Gln Thr Ile Trp Lys Glu

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Met Gly

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atc ggg aag tct aaa ata aat tcc tgc cct ctt tct ctc tct tgg ggt 164

Ile Gly Lys Ser Lys Ile Asn Ser Cys Pro Leu Ser Leu Ser Trp Gly

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10

15

aaa agg cac agt gtg gat aca agt cca gga tat cat gag tca gat tcc 212

Lys Arg His Ser Val Asp Thr Ser Pro Gly Tyr His Glu Ser Asp Ser

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25

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aag aag tct gaa gat cta tcc ttg tgt aat gtt gct gag cac agc aat 260

Lys Lys Ser Glu Asp Leu Ser Leu Cys Asn Val Ala Glu His Ser Asn

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aca aca gag ggg cca aca gga aag cag gag gga gct cag agc gtg gaa 308

Thr Thr Glu Gly Pro Thr Gly Lys Gln Glu Gly Ala Gln Ser Val Glu

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65

gag atg ttt gaa gaa gaa gct gaa gaa gag gtg ttc ctc aaa ttt gtg 356

Glu Met Phe Glu Glu Glu Ala Glu Glu Glu Val Phe Leu Lys Phe Val

70

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ata ttg cat gca gaa gat gac aca gat gaa gcc ctc aga gtc cag aat 404

Ile Leu His Ala Glu Asp Asp Thr Asp Glu Ala Leu Arg Val Gln Asn

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90

95

ctg cta caa gat gac ttt ggt atc aaa ccc gga ata atc ttt gct gag 452

Leu Leu Gln Asp Asp Phe Gly Ile Lys Pro Gly Ile Ile Phe Ala Glu

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105

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atg cca tgt ggc aga cag cat tta cag aat tta gat gat gct gta aat 500

Met Pro Cys Gly Arg Gln His Leu Gln Asn Leu Asp Asp Ala Val Asn

115

120

125

130

ggg tct gca tgg aca atc tta tta ctg act gaa aac ttt tta aga gat 548

Gly Ser Ala Trp Thr Ile Leu Leu Leu Thr Glu Asn Phe Leu Arg Asp

135

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act tgg tgt aat ttc cag ttc tat acg tcc cta atg aac tcc gtt aac 596

Thr Trp Cys Asn Phe Gln Phe Tyr Thr Ser Leu Met Asn Ser Val Asn

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agg cag cat aaa tac aac tct gtt ata ccc atg cgg ccc ctg aac aat 644

Arg Gln His Lys Tyr Asn Ser Val Ile Pro Met Arg Pro Leu Asn Asn

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ccc ctt ccc cga gaa agg act ccc ttt gcc ctc caa acc atc aat gcc 692

Pro Leu Pro Arg Glu Arg Thr Pro Phe Ala Leu Gln Thr Ile Asn Ala

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185

190

tta gag gaa gaa agt cgt gga ttt cct aca caa gta gaa aga att ttt 740

Leu Glu Glu Glu Ser Arg Gly Phe Pro Thr Gln Val Glu Arg Ile Phe

195

200

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210

cag gag tct gtg tat aag aca caa caa act ata tgg aaa gag aca aga 788

Gln Glu Ser Val Tyr Lys Thr Gln Gln Thr Ile Trp Lys Glu Thr Arg

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225

aat atg gta caa aga caa ttt att gcc tgagatgaaa catataacat 835

Asn Met Val Gln Arg Gln Phe Ile Ala

230

235

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<400> 89

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35 40 45

Tyr Phe Ser Leu Leu Asn Glu Lys Ala Thr Asn Val Pro Phe Val Leu

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Ile Ala Thr Gly Thr Val Ile Ile Leu Leu Gly Thr Phe Gly Cys Phe

65 70 75 80

Ala Thr Cys Arg Ala Ser Ala Trp Met Leu Lys Leu Tyr Ala Met Phe

85 90 95

Leu Thr Leu Val Phe Leu Val Glu Leu Val Ala Ala Ile Val Gly Phe

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Met Ala Ser Pro Ser Arg Arg Leu Gln Thr Lys Pro Val Ile Thr Cys

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Phe Lys Ser Val Leu Leu Ile Tyr Thr Phe Ile Phe Trp Ile Thr Gly

20 25 30

gtt atc ctt ctt gca gtt ggc att tgg ggc aag gtg agc ctg gag aat 203

Val Ile Leu Leu Ala Val Gly Ile Trp Gly Lys Val Ser Leu Glu Asn

35 40 45

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Tyr Phe Ser Leu Leu Asn Glu Lys Ala Thr Asn Val Pro Phe Val Leu

50 55 60

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Ile Ala Thr Gly Thr Val Ile Ile Leu Leu Gly Thr Phe Gly Cys Phe

65 70 75 80

gct acc tgc cga gct tct gca tgg atg cta aaa ctg tat gca atg ttt 347

Ala Thr Cys Arg Ala Ser Ala Trp Met Leu Lys Leu Tyr Ala Met Phe

85 90 95

ctg act ctc gtt ttt ttg gtc gaa ctg gtc gct gcc atc gta gga ttt 395

Leu Thr Leu Val Phe Leu Val Glu Leu Val Ala Ala Ile Val Gly Phe

100

105

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Val Phe Arg His Glu Ile Lys Asn Ser Phe Lys Asn Asn Tyr Glu Lys

115

120

125

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Ala Leu Lys Gln Tyr Asn Ser Thr Gly Asp Tyr Arg Ser His Ala Val

130

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gac aag atc caa aat acg ttg cat tgt tgt ggt gtc acc gat tat aga 539

Asp Lys Ile Gln Asn Thr Leu His Cys Cys Gly Val Thr Asp Tyr Arg

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gat tgg aca gat act aat tat tac tca gaa aaa gga ttt cct aag agt 587

Asp Trp Thr Asp Thr Asn Tyr Tyr Ser Glu Lys Gly Phe Pro Lys Ser

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170

175

tgc tgt aaa ctt gaa gat tgt act cca cag aga gat gca gac aaa gta 635

Cys Cys Lys Leu Glu Asp Cys Thr Pro Gln Arg Asp Ala Asp Lys Val

180

185

190

aac aat gaa ggt tgt ttt ata aag gtg atg acc att ata gag tca gaa 683

Asn Asn Glu Gly Cys Phe Ile Lys Val Met Thr Ile Ile Glu Ser Glu

195

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Met Gly Val Val Ala Gly Ile Ser Phe Gly Val Ala Cys Phe Gln Leu

210 215 220

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Ile Gly Ile Phe Leu Ala Tyr Cys Leu Ser Arg Ala Ile Thr Asn Asn

225 230 235 240

cag tat gag ata gtg taaccaaatg tatctgtggg cctattcctc tctaccttta 834

Gln Tyr Glu Ile Val

245

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gattgtataa tttgcaccaa gaagttaaaa tgttttatga ctctctgttc tgctgacagg 1374

35

40

45

Asn Ser Glu Ala Cys Arg Asp Gly Leu Arg Ala Val Met Glu Cys Arg

50

55

60

Asn Val Thr His Leu Leu Gln Gln Glu Leu Thr Glu Ala Gln Lys Gly

65

70

75

80

Phe Gln Asp Val Glu Ala Gln Ala Ala Thr Cys Asn His Thr Val Met

85

90

95

Ala Leu Met Ala Ser Leu Asp Ala Glu Lys Ala Gln Gly Gln Lys Lys

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105

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Val Glu Glu Leu Glu Gly Glu Ile Thr Thr Leu Asn His Lys Leu Gln

115

120

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Asp Ala Ser Ala Glu Val Glu Arg Leu Arg Arg Glu Asn Gln Val Leu

130

135

140

Ser Val Arg Ile Ala Asp Lys Lys Tyr Tyr Pro Ser Ser Gln Asp Ser

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165

170

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Ala Leu Leu Gln

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<222> (26).. (565)

<400> 92

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Arg Val Pro Met Glu Asp Gly Asp Lys Arg Cys Lys Leu Leu Leu Gly

10

15

20

25

ata gga att ctg gtg ctc ctg atc atc gtg att ctg ggg gtg ccc ttg 148

Ile Gly Ile Leu Val Leu Leu Ile Ile Val Ile Leu Gly Val Pro Leu

30

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att atc ttc acc atc aag gcc aac agc gag gcc tgc cgg gac ggc ctt 196

Ile Ile Phe Thr Ile Lys Ala Asn Ser Glu Ala Cys Arg Asp Gly Leu

45

50

55

cgg gca gtg atg gag tgt cgc aat gtc acc cat ctc ctg caa caa gag 244

Arg Ala Val Met Glu Cys Arg Asn Val Thr His Leu Leu Gln Gln Glu

60

65

70

ctg acc gag gcc cag aag ggc ttt cag gat gtg gag gcc cag gct gcc 292
 Leu Thr Glu Ala Gln Lys Gly Phe Gln Asp Val Glu Ala Gln Ala Ala
 75 80 85

acc tgc aac cac act gtg atg gcc cta atg gct tcc ctg gat gca gag 340
 Thr Cys Asn His Thr Val Met Ala Leu Met Ala Ser Leu Asp Ala Glu
 90 95 100 105

aag gcc caa gga caa aag aaa gtg gag gag ctt gag gga gag atc act 388
 Lys Ala Gln Gly Gln Lys Lys Val Glu Glu Leu Glu Gly Glu Ile Thr
 110 115 120

aca tta aac cat aag ctt cag gac gcg tct gca gag gtg gag cga ctg 436
 Thr Leu Asn His Lys Leu Gln Asp Ala Ser Ala Glu Val Glu Arg Leu
 125 130 135

aga aga gaa aac cag gtc tta agc gtg aga atc gcg gac aag aag tac 484
 Arg Arg Glu Asn Gln Val Leu Ser Val Arg Ile Ala Asp Lys Lys Tyr
 140 145 150

tac ccc agc tcc cag gac tcc agc tcc gct gcg gcg ccc cag ctg ctg 532
 Tyr Pro Ser Ser Gln Asp Ser Ser Ser Ala Ala Ala Pro Gln Leu Leu
 155 160 165

att gtg ctg ctg ggc ctc agc gct ctg ctg cag tgagatccca ggaagctggc 585
 Ile Val Leu Leu Gly Leu Ser Ala Leu Leu Gln
 170 175 180

acatcttgga aggtccgtcc tgctcggtt ttcgttgaa cattcccttg atctcatcag 645

ttctgagcgg gtcattggggc aacacgggta gcggggagag cacggggtag ccggagaagg 705

gcctctggag caggtctgga ggggccatgg ggcagtcctg ggtgtgggga cacagtcggg 765

ttgaccagg gctgtctccc tccagagcct ccctccggac aatgagtccc ccctcttgtc 825

tcccacctg agattgggca tgggggtgcgg tgtggggggc atgtgctgcc tgttgttatg 885

ggtttttttt gcgggggggg ttgctttttt ctgggggtctt tgagctccaa aaaataaaca 945

cttcctttga gggagagcac acctt 970

- <210> 93
- <211> 331
- <212> PRT
- <213> Homo sapiens

<400> 93

Met Asp Ser Glu Lys Lys Arg Phe Thr Glu Glu Ala Thr Lys Tyr Phe

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Arg Glu Arg Val Ser Pro Val His Leu Gln Ile Leu Leu Thr Asn Asn

20 25 30

Glu Ala Trp Lys Arg Phe Val Thr Ala Ala Glu Leu Pro Arg Asp Glu



45

60

80

95

110

125

140

160

175

190

Lys Val Phe Lys Glu Val Met Arg Asp Ile Thr Pro Asn Leu Leu Ser

195

200

205

Leu Leu Asn Asn Tyr Tyr Glu Ala Thr Gln Thr Ile Gly Ser Glu Ile

210

215

220

Arg Ala Ile Arg Gln Ala Arg Ala Arg Ala Arg Leu Pro Val Thr Thr

225

230

235

240

Trp Arg Ile Ser Ala Gly Ser Gly Gly Gln Ala Glu Arg Thr Ile Ala

245

250

255

Gly Thr Thr Arg Ala Val Ser Arg Gly Ala Arg Ile Leu Ser Ala Thr

260

265

270

Thr Ser Gly Ile Phe Leu Ala Leu Asp Val Val Asn Leu Val Tyr Glu

275

280

285

Ser Lys His Leu His Glu Gly Ala Lys Ser Ala Ser Ala Glu Glu Leu

290

295

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Arg Arg Gln Ala Gln Glu Leu Glu Glu Asn Leu Met Glu Leu Thr Gln

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Ile Tyr Gln Arg Leu Asn Pro Cys His Thr His

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<211> 2039

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<213> Homo sapiens

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<221> CDS

<222> (175).. (1167)

<400> 94

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tcagtgactg gagagctcca aggaaagtct ctcagtgacc tggctgctgg cacc atg 177

Met

1

gac tca gaa aag aaa cgc ttt act gaa gag gcc acc aaa tac ttc cgg 225

Asp Ser Glu Lys Lys Arg Phe Thr Glu Glu Ala Thr Lys Tyr Phe Arg

5

10

15

gag aga gtc agc cca gtg cat ctg caa atc ctg ctg act aac aat gaa 273

Glu Arg Val Ser Pro Val His Leu Gln Ile Leu Leu Thr Asn Asn Glu

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25

30

gcc tgg aag aga ttc gtg act gcg gct gaa ttg ccc agg gat gag gca 321

Ala Trp Lys Arg Phe Val Thr Ala Ala Glu Leu Pro Arg Asp Glu Ala

35

40

45

Thr Gly Ile Thr Thr Ser Ile Val Glu His Ser Tyr Thr Ser Ser Ala

165

170

175

gaa gct gaa gcc agc agg ctg act gca acc agc att gac cga ttg aag 753

Glu Ala Glu Ala Ser Arg Leu Thr Ala Thr Ser Ile Asp Arg Leu Lys

180

185

190

gta ttt aag gaa gtt atg cgt gac atc aca ccc aac tta ctt tcc ctt 801

Val Phe Lys Glu Val Met Arg Asp Ile Thr Pro Asn Leu Leu Ser Leu

195

200

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ctt aat aat tat tac gaa gcc aca caa acc att ggg agt gaa atc cgt 849

Leu Asn Asn Tyr Tyr Glu Ala Thr Gln Thr Ile Gly Ser Glu Ile Arg

210

215

220

225

gcc atc agg caa gcc aga gcc agg gcc cga ctc cct gtg acc acc tgg 897

Ala Ile Arg Gln Ala Arg Ala Arg Ala Arg Leu Pro Val Thr Thr Trp

230

235

240

cga atc tca gct gga agt ggt ggt caa gca gag aga acg att gca ggc 945

Arg Ile Ser Ala Gly Ser Gly Gly Gln Ala Glu Arg Thr Ile Ala Gly

245

250

255

acc acc cgg gca gtg agc aga gga gcc cgg atc ctg agt gcg acc act 993

Thr Thr Arg Ala Val Ser Arg Gly Ala Arg Ile Leu Ser Ala Thr Thr

260

265

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tca ggc atc ttc ctt gca ctg gat gtg gtc aac ctt gta tac gag tca 1041

Ser Gly Ile Phe Leu Ala Leu Asp Val Val Asn Leu Val Tyr Glu Ser

ctgtcttgtc ctcttggaag tgtatctcag tcagccagtg gcttcttgat gatggcgggtg 1727

gaggtggtgg ttgtagtgtg atggatcccc tttagggttat ttaggggtat atgtcccctg 1787

cttgaaccct gaaggccagg taatgagcca tggccattgt cccagctga ggaccaggtg 1847

tctctaaaaa cccaaacatc ctggagagta tgcgagaacc taccaagaaa aacagtctca 1907

ttactcatat acagcaggca aagagacaga aaattaactg aaaagcagtt tagagactgg 1967

gggaggccgg atctctagag ccactctgct gagtgccctg tgtgtaagtc ctaataaact 2027

cacctactca cc 2039

<210> 95

<211> 407

<212> PRT

<213> Homo sapiens

<400> 95

Met Glu Leu Leu Glu Glu Asp Leu Thr Cys Pro Ile Cys Cys Ser Leu

1

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15

Phe Asp Asp Pro Arg Val Leu Pro Cys Ser His Asn Phe Cys Lys Lys

20

25

30

Cys Leu Glu Gly Ile Leu Glu Gly Ser Val Arg Asn Ser Leu Trp Arg

all amino acids are present in the protein

35

40

45

Pro Ala Pro Phe Lys Cys Pro Thr Cys Arg Lys Glu Thr Ser Ala Thr

50

55

60

Gly Ile Asn Ser Leu Gln Val Asn Tyr Ser Leu Lys Gly Ile Val Glu

65

70

75

80

Lys Tyr Asn Lys Ile Lys Ile Ser Pro Lys Met Pro Val Cys Lys Gly

85

90

95

His Leu Gly Gln Pro Leu Asn Ile Phe Cys Leu Thr Asp Met Gln Leu

100

105

110

Ile Cys Gly Ile Cys Ala Thr Arg Gly Glu His Thr Lys His Val Phe

115

120

125

Cys Ser Ile Glu Asp Ala Tyr Ala Gln Glu Arg Asp Ala Phe Glu Ser

130

135

140

Leu Phe Gln Ser Phe Glu Thr Trp Arg Arg Gly Asp Ala Leu Ser Arg

145

150

155

160

Leu Asp Thr Leu Glu Thr Ser Lys Arg Lys Ser Leu Gln Leu Leu Thr

165

170

175

Lys Asp Ser Asp Lys Val Lys Glu Phe Phe Glu Lys Leu Gln His Thr

180

185

190

Leu Asp Gln Lys Lys Asn Glu Ile Leu Ser Asp Phe Glu Thr Met Lys
 195 200 205

Leu Ala Val Met Gln Ala Tyr Asp Pro Glu Ile Asn Lys Leu Asn Thr
 210 215 220

Ile Leu Gln Glu Gln Arg Met Ala Phe Asn Ile Ala Glu Ala Phe Lys
 225 230 235 240

Asp Val Ser Glu Pro Ile Val Phe Leu Gln Gln Met Gln Glu Phe Arg
 245 250 255

Glu Lys Ile Lys Val Ile Lys Glu Thr Pro Leu Pro Pro Ser Asn Leu
 260 265 270

Pro Ala Ser Pro Leu Met Lys Asn Phe Asp Thr Ser Gln Trp Glu Asp
 275 280 285

Ile Lys Leu Val Asp Val Asp Lys Leu Ser Leu Pro Gln Asp Thr Gly
 290 295 300

Thr Phe Ile Ser Lys Ile Pro Trp Ser Phe Tyr Lys Leu Phe Leu Leu
 305 310 315 320

Ile Leu Leu Leu Gly Leu Val Ile Val Phe Gly Pro Thr Met Phe Leu
 325 330 335

Glu Trp Ser Leu Phe Asp Asp Leu Ala Thr Trp Lys Gly Cys Leu Ser
 340 345 350

355 360 365

370 375 380

385 390 395 400

405

<211> 1409

⟨213⟩ Homo sapiens

<221> CDS

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tttggcctgg gaaatagtaa ccctgccaaa tacatcagct tgtaggagac agaggatgtg 180

atg gag ctg ctt gaa gaa gat ctc aca tgc cct att tgt tgt agt ctg 228

Met Glu Leu Leu Glu Glu Asp Leu Thr Cys Pro Ile Cys Cys Ser Leu

1

5

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15

ttt gat gat cca cgg gtt ttg cct tgc tcc cac aac ttc tgc aaa aaa 276

Phe Asp Asp Pro Arg Val Leu Pro Cys Ser His Asn Phe Cys Lys Lys

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25

30

tgc tta gaa ggt atc tta gaa ggg agt gtg cgg aat tcc ttg tgg aga 324

Cys Leu Glu Gly Ile Leu Glu Gly Ser Val Arg Asn Ser Leu Trp Arg

35

40

45

cca gct cca ttc aag tgt cct aca tgc cgt aag gaa act tca gct act 372

Pro Ala Pro Phe Lys Cys Pro Thr Cys Arg Lys Glu Thr Ser Ala Thr

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55

60

gga att aat agc ctg cag gtt aat tac tcc ctg aag ggt att gtg gaa 420

Gly Ile Asn Ser Leu Gln Val Asn Tyr Ser Leu Lys Gly Ile Val Glu

65

70

75

80

aag tat aac aag atc aag atc tct ccc aaa atg cca gta tgc aaa gga 468

Lys Tyr Asn Lys Ile Lys Ile Ser Pro Lys Met Pro Val Cys Lys Gly

85

90

95

cac ttg ggg cag cct ctc aac att ttc tgc ctg act gat atg cag ctg 516

His Leu Gly Gln Pro Leu Asn Ile Phe Cys Leu Thr Asp Met Gln Leu

100

105

110

att tgt ggg atc tgt gct act cgt ggg gag cac acc aaa cat gtc ttc 564

Ile Cys Gly Ile Cys Ala Thr Arg Gly Glu His Thr Lys His Val Phe

115

120

125

tgt tct att gaa gat gcc tat gct cag gaa agg gat gcc ttt gag tcc 612

Cys Ser Ile Glu Asp Ala Tyr Ala Gln Glu Arg Asp Ala Phe Glu Ser

130

135

140

ctc ttc cag agc ttt gag acc tgg cgt cgg gga gat gct ctt tct cgc 660

Leu Phe Gln Ser Phe Glu Thr Trp Arg Arg Gly Asp Ala Leu Ser Arg

145

150

155

160

ttg gat acc ttg gaa act agt aag agg aaa tcc cta cag tta ctg act 708

Leu Asp Thr Leu Glu Thr Ser Lys Arg Lys Ser Leu Gln Leu Leu Thr

165

170

175

aaa gat tca gat aaa gtg aag gaa ttt ttt gag aag tta caa cac aca 756

Lys Asp Ser Asp Lys Val Lys Glu Phe Phe Glu Lys Leu Gln His Thr

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185

190

ctg gat caa aag aag aat gaa att ctg tct gac ttt gag acc atg aaa 804

Leu Asp Gln Lys Lys Asn Glu Ile Leu Ser Asp Phe Glu Thr Met Lys

195

200

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ctt gct gtt atg caa gca tat gac cca gag atc aac aaa ctc aac acc 852

Leu Ala Val Met Gln Ala Tyr Asp Pro Glu Ile Asn Lys Leu Asn Thr

210

215

220

atc ttg cag gag caa cgg atg gcc ttt aac att gct gag gct ttc aaa 900

Ile Leu Gln Glu Gln Arg Met Ala Phe Asn Ile Ala Glu Ala Phe Lys
 225 230 235 240

gat gtg tca gaa ccc att gta ttt ctg caa cag atg cag gag ttt aga 948
 Asp Val Ser Glu Pro Ile Val Phe Leu Gln Gln Met Gln Glu Phe Arg
 245 250 255

gag aaa atc aaa gta atc aag gaa act cct tta cct ccc tct aat ttg 996
 Glu Lys Ile Lys Val Ile Lys Glu Thr Pro Leu Pro Pro Ser Asn Leu
 260 265 270

cct gca agc cct tta atg aag aac ttt gat acc agt cag tgg gaa gac 1044
 Pro Ala Ser Pro Leu Met Lys Asn Phe Asp Thr Ser Gln Trp Glu Asp
 275 280 285

ata aaa cta gtc gat gtg gat aaa ctt tct ttg cct caa gac act ggc 1092
 Ile Lys Leu Val Asp Val Asp Lys Leu Ser Leu Pro Gln Asp Thr Gly
 290 295 300

aca ttc att agc aag att ccc tgg agc ttt tat aag tta ttt ttg cta 1140
 Thr Phe Ile Ser Lys Ile Pro Trp Ser Phe Tyr Lys Leu Phe Leu Leu
 305 310 315 320

atc ctt ctg ctt ggc ctt gtc att gtc ttt ggt cct acc atg ttc cta 1188
 Ile Leu Leu Leu Gly Leu Val Ile Val Phe Gly Pro Thr Met Phe Leu
 325 330 335

gaa tgg tca tta ttt gat gac ctg gca act tgg aaa ggc tgt ctt tca 1236
 Glu Trp Ser Leu Phe Asp Asp Leu Ala Thr Trp Lys Gly Cys Leu Ser
 332/735

340

345

350

aac ttc agt tcc tat ctg act aaa aca gcc gat ttc ata gaa caa tca 1284

Asn Phe Ser Ser Tyr Leu Thr Lys Thr Ala Asp Phe Ile Glu Gln Ser

355

360

365

gtt ttt tac tgg gaa cag gtg aca gat ggg ttt ttc att ttc aat gaa 1332

Val Phe Tyr Trp Glu Gln Val Thr Asp Gly Phe Phe Ile Phe Asn Glu

370

375

380

aga ttc aag aat ttt act ttg gtg gta ctg aac aat gtg gca gaa ttt 1380

Arg Phe Lys Asn Phe Thr Leu Val Val Leu Asn Asn Val Ala Glu Phe

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395

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gtg tgc aaa tat aaa cta tta taaaatcg

1409

Val Cys Lys Tyr Lys Leu Leu

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<210> 97

<211> 465

<212> PRT

<213> Homo sapiens

<400> 97

Met Ala Ser Thr Thr Ser Thr Lys Lys Met Met Glu Glu Ala Thr Cys

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Ser Ile Cys Leu Ser Leu Met Thr Asn Pro Val Ser Ile Asn Cys Gly

333/735

20

25

30

His Ser Tyr Cys His Leu Cys Ile Thr Asp Phe Phe Lys Asn Pro Ser

35

40

45

Gln Lys Gln Leu Arg Gln Glu Thr Phe Cys Cys Pro Gln Cys Arg Ala

50

55

60

Pro Phe His Met Asp Ser Leu Arg Pro Asn Lys Gln Leu Gly Ser Leu

65

70

75

80

Ile Glu Ala Leu Lys Glu Thr Asp Gln Glu Met Ser Cys Glu Glu His

85

90

95

Gly Glu Gln Phe His Leu Phe Cys Glu Asp Glu Gly Gln Leu Ile Cys

100

105

110

Trp Arg Cys Glu Arg Ala Pro Gln His Lys Gly His Thr Thr Ala Leu

115

120

125

Val Glu Asp Val Cys Gln Gly Tyr Lys Glu Lys Leu Gln Glu Ala Val

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Thr Lys Leu Lys Gln Leu Glu Asp Arg Cys Thr Glu Gln Lys Leu Ser

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Thr Ala Met Arg Ile Thr Lys Trp Lys Glu Lys Val Gln Ile Gln Arg

165

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175

Gln Lys Ile Arg Ser Asp Phe Lys Asn Leu Gln Cys Phe Leu His Glu
180 185 190

Glu Glu Lys Ser Tyr Leu Trp Arg Leu Glu Lys Glu Glu Gln Gln Thr
195 200 205

Leu Ser Arg Leu Arg Asp Tyr Glu Ala Gly Leu Gly Leu Lys Ser Asn
210 215 220

Glu Leu Lys Ser His Ile Leu Glu Leu Glu Glu Lys Cys Gln Gly Ser
225 230 235 240

Ala Gln Lys Leu Leu Gln Asn Val Asn Asp Thr Leu Ser Arg Ser Trp
245 250 255

Ala Val Lys Leu Glu Thr Ser Glu Ala Val Ser Leu Glu Leu His Thr
260 265 270

Met Cys Asn Val Ser Lys Leu Tyr Phe Asp Val Lys Lys Met Leu Arg
275 280 285

Ser His Gln Val Ser Val Thr Leu Asp Pro Asp Thr Ala His His Glu
290 295 300

Leu Ile Leu Ser Glu Asp Arg Arg Gln Val Thr Arg Gly Tyr Thr Gln
305 310 315 320

Glu Asn Gln Asp Thr Ser Ser Arg Arg Phe Thr Ala Phe Pro Cys Val
325 330 335

Leu Gly Cys Glu Gly Phe Thr Ser Gly Arg Arg Tyr Phe Glu Val Asp
 340 345 350

Val Gly Glu Gly Thr Gly Trp Asp Leu Gly Val Cys Met Glu Asn Val
 355 360 365

Gln Arg Gly Thr Gly Met Lys Gln Glu Pro Gln Ser Gly Phe Trp Thr
 370 375 380

Leu Arg Leu Cys Lys Lys Lys Gly Tyr Val Ala Leu Thr Ser Pro Pro
 385 390 395 400

Thr Ser Leu His Leu His Glu Gln Pro Leu Leu Val Gly Ile Phe Leu
 405 410 415

Asp Tyr Glu Ala Gly Val Val Ser Phe Tyr Asn Gly Asn Thr Gly Cys
 420 425 430

His Ile Phe Thr Phe Pro Lys Ala Ser Phe Ser Asp Thr Leu Arg Pro
 435 440 445

Tyr Phe Gln Val Tyr Gln Tyr Ser Pro Leu Phe Leu Pro Pro Pro Gly
 450 455 460

Asp
 465

<210> 98

<211> 1940

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (477).. (1871)

<400> 98

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ccttggaagg aggggagccc catctcccca gaagagcagt gaccccagca gagagggggc 180

tggtgtatca ctggaggaaa tagcctgcc aggaatacac gtcttcagaa gaagttctgt 240

gtggettcaa gagactgac aaattgtgag aggaaaacag cctaccgggt cctcttttct 300

tcaatacaaa atgagataat aggggttgga aggaaaacct tcaagaccta tggaagtcag 360

ttgcagccag ctcatcacat agaggtgcag gtgaggtgta ttttcatcac ggtggaaaat 420

tctggctgct tcattccat ctctagagcc aatattggag cttttcaata aaagct atg 479

Met

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gcc tca acc acc agc acc aag aag atg atg gag gaa gcc acc tgc tcc 527

[illegible]

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Ile Cys Leu Ser Leu Met Thr Asn Pro Val Ser Ile Asn Cys Gly His

25

30

Ser Tyr Cys His Leu Cys Ile Thr Asp Phe Phe Lys Asn Pro Ser Gln

40

45

Lys Gln Leu Arg Gln Glu Thr Phe Cys Cys Pro Gln Cys Arg Ala Pro

55

60

65

Phe His Met Asp Ser Leu Arg Pro Asn Lys Gln Leu Gly Ser Leu Ile

75

80

Glu Ala Leu Lys Glu Thr Asp Gln Glu Met Ser Cys Glu Glu His Gly

90

95

Glu Gln Phe His Leu Phe Cys Glu Asp Glu Gly Gln Leu Ile Cys Trp

105

110

Arg Cys Glu Arg Ala Pro Gln His Lys Gly His Thr Thr Ala Leu Val

115

120

125

gaa gac gta tgc cag ggc tac aag gaa aag ctc cag gaa gct gtg aca 911

Glu Asp Val Cys Gln Gly Tyr Lys Glu Lys Leu Gln Glu Ala Val Thr

130

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140

145

aaa ctg aag caa ctt gaa gac aga tgt acg gag cag aag ctg tcc aca 959

Lys Leu Lys Gln Leu Glu Asp Arg Cys Thr Glu Gln Lys Leu Ser Thr

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160

gca atg cga ata act aaa tgg aaa gag aag gta cag att cag aga caa 1007

Ala Met Arg Ile Thr Lys Trp Lys Glu Lys Val Gln Ile Gln Arg Gln

165

170

175

aaa atc cgg tct gac ttt aag aat ctc cag tgt ttc cta cat gag gaa 1055

Lys Ile Arg Ser Asp Phe Lys Asn Leu Gln Cys Phe Leu His Glu Glu

180

185

190

gag aag tct tat ctc tgg agg ctg gag aaa gaa gaa caa cag act ctg 1103

Glu Lys Ser Tyr Leu Trp Arg Leu Glu Lys Glu Glu Gln Gln Thr Leu

195

200

205

agt aga ctg agg gac tat gag gct ggt ctg ggg ctg aag agc aat gaa 1151

Ser Arg Leu Arg Asp Tyr Glu Ala Gly Leu Gly Leu Lys Ser Asn Glu

210

215

220

225

ctc aag agc cac atc ctg gaa ctg gag gaa aaa tgt cag ggc tca gcc 1199

Leu Lys Ser His Ile Leu Glu Leu Glu Glu Lys Cys Gln Gly Ser Ala

230

235

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cag aaa ttg ctg cag aat gtg aat gac act ttg agc agg agt tgg gct 1247

Gln Lys Leu Leu Gln Asn Val Asn Asp Thr Leu Ser Arg Ser Trp Ala

245

250

255

gtg aag ctg gaa aca tca gag gct gtc tcc ttg gaa ctt cat act atg 1295

Val Lys Leu Glu Thr Ser Glu Ala Val Ser Leu Glu Leu His Thr Met

260

265

270

tgc aat gtt tcc aag ctt tac ttc gat gtg aag aaa atg tta agg agt 1343

Cys Asn Val Ser Lys Leu Tyr Phe Asp Val Lys Lys Met Leu Arg Ser

275

280

285

cat caa gtt agt gtg act ctg gat cca gat aca gct cat cac gaa cta 1391

His Gln Val Ser Val Thr Leu Asp Pro Asp Thr Ala His His Glu Leu

290

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att ctc tct gag gat cgg aga caa gtg act cgt gga tac acc cag gag 1439

Ile Leu Ser Glu Asp Arg Arg Gln Val Thr Arg Gly Tyr Thr Gln Glu

310

315

320

aat cag gac aca tct tcc agg aga ttt act gcc ttc ccc tgt gtc ttg 1487

Asn Gln Asp Thr Ser Ser Arg Arg Phe Thr Ala Phe Pro Cys Val Leu

325

330

335

ggt tgt gaa ggc ttc acc tca gga aga cgt tac ttt gaa gtg gat gtt 1535

Gly Cys Glu Gly Phe Thr Ser Gly Arg Arg Tyr Phe Glu Val Asp Val

340

345

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ggc gaa gga acc gga tgg gat tta gga gtt tgt atg gaa aat gtg cag 1583

Gly Glu Gly Thr Gly Trp Asp Leu Gly Val Cys Met Glu Asn Val Gln

355

360

365

agg ggc act ggc atg aag caa gag cct cag tct gga ttc tgg acc ctc 1631

Arg Gly Thr Gly Met Lys Gln Glu Pro Gln Ser Gly Phe Trp Thr Leu

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375

380

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agg ctg tgc aaa aag aaa ggc tat gta gca ctt act tct ccc cca act 1679

Arg Leu Cys Lys Lys Lys Gly Tyr Val Ala Leu Thr Ser Pro Pro Thr

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395

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tcc ctt cat ctg cat gag cag ccc ctg ctt gtg gga att ttt ctg gac 1727

Ser Leu His Leu His Glu Gln Pro Leu Leu Val Gly Ile Phe Leu Asp

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410

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tat gag gcc gga gtt gta tcc ttt tat aac ggg aat act ggc tgc cac 1775

Tyr Glu Ala Gly Val Val Ser Phe Tyr Asn Gly Asn Thr Gly Cys His

420

425

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atc ttt act ttc ccg aag gct tcc ttc tct gat act ctc cgg ccc tat 1823

Ile Phe Thr Phe Pro Lys Ala Ser Phe Ser Asp Thr Leu Arg Pro Tyr

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440

445

ttc cag gtt tat caa tat tct cct ttg ttt ctg cct ccc cca ggt gac 1871

Phe Gln Val Tyr Gln Tyr Ser Pro Leu Phe Leu Pro Pro Pro Gly Asp

450

455

460

465

taaggaaaag agcagaagct ccttggttta accagcacag agaaaataat ataaatccca 1931

100

105

110

Trp Arg Cys Glu Arg Ala Pro Gln His Lys Gly His Thr Thr Ala Leu

115

120

125

Val Glu Asp Val Cys Gln Gly Tyr Lys Glu Lys Leu Gln Lys Ala Val

130

135

140

Thr Lys Leu Lys Gln Leu Glu Asp Arg Cys Thr Glu Gln Lys Leu Ser

145

150

155

160

Thr Ala Met Arg Ile Thr Lys Trp Lys Glu Lys Val Gln Ile Gln Arg

165

170

175

Gln Lys Ile Arg Ser Asp Phe Lys Asn Leu Gln Cys Phe Leu His Glu

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185

190

Glu Glu Lys Ser Tyr Leu Trp Arg Leu Glu Lys Glu Glu Gln Gln Thr

195

200

205

Leu Ser Arg Leu Arg Asp Tyr Glu Ala Gly Leu Gly Leu Lys Ser Asn

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215

220

Glu Leu Lys Ser His Ile Leu Glu Leu Glu Glu Lys Cys Gln Gly Ser

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230

235

240

Ala Gln Lys Leu Leu Gln Asn Val Asn Asp Thr Leu Ser Arg Ser Trp

245

250

255

Ala Val Lys Leu Glu Thr Ser Glu Ala Val Ser Leu Glu Leu His Thr
260 265 270

Met Cys Asn Val Ser Lys Leu Tyr Phe Asp Val Lys Lys Met Leu Arg
275 280 285

Ser His Gln Val Ser Val Thr Leu Asp Pro Asp Thr Ala His His Glu
290 295 300

Leu Ile Leu Ser Glu Asp Arg Arg Gln Val Thr Arg Gly Tyr Thr Gln
305 310 315 320

Glu Asn Gln Asp Thr Ser Ser Arg Arg Phe Thr Ala Phe Pro Cys Val
325 330 335

Leu Gly Cys Glu Gly Phe Thr Ser Gly Arg Arg Tyr Phe Glu Val Asp
340 345 350

Val Gly Glu Gly Thr Gly Trp Asp Leu Gly Val Cys Met Glu Asn Val
355 360 365

Gln Arg Gly Thr Gly Met Lys Gln Glu Pro Gln Ser Gly Phe Trp Thr
370 375 380

Leu Arg Leu Cys Lys Lys Lys Gly Tyr Val Ala Leu Thr Ser Pro Pro
385 390 395 400

Thr Ser Leu His Leu His Glu Gln Pro Leu Leu Val Gly Ile Phe Leu
405 410 415

Asp Tyr Glu Ala Gly Val Val Ser Phe Tyr Asn Gly Asn Thr Gly Cys

420

425

430

His Ile Phe Thr Phe Pro Lys Ala Ser Phe Ser Asp Thr Leu Arg Pro

435

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445

Tyr Phe Gln Val Tyr Gln Tyr Ser Pro Leu Phe Leu Pro Pro Pro Gly

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455

460

Asp

465

<210> 100

<211> 1940

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (477).. (1871)

<400> 100

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ccttgaagg aggggagccc catctcccca gaagagcagt gacccagca gagaggggcc 180

tggtgtatca ctggaggaaa tagcctgcc aggaatacac gtcttcagaa gaagttctgt 240

gtggcttcaa gagactgac aaattgtgag aggaaaacag cctaccgggt cctcttttct 300

tcaatacaaa atgagataat aggggttgga aggaaaacct tcaagaccta tggaagtcag 360

ttgcagccag ctcatcacat agaggtgcag gtgaggtgta ttttcatcac ggtggaaaat 420

tctggtgtgt tcattccat ctctagagcc aatattggag cttttcaata aaagct atg 479

Met

1

gcc tca acc acc agc acc aag aag atg atg gag gaa gcc acc tgc tcc 527

Ala Ser Thr Thr Ser Thr Lys Lys Met Met Glu Glu Ala Thr Cys Ser

5

10

15

atc tgc ctg agc ctg atg acg aac cca gta agc atc aac tgt gga cac 575

Ile Cys Leu Ser Leu Met Thr Asn Pro Val Ser Ile Asn Cys Gly His

20

25

30

agc tac tgc cac ttg tgt ata aca gac ttc ttt aaa aac cca agc caa 623

Ser Tyr Cys His Leu Cys Ile Thr Asp Phe Phe Lys Asn Pro Ser Gln

35

40

45

aag caa ctg agg cag gag aca ttc tgc tgt ccc cag tgt cgg gct cca 671

Lys Gln Leu Arg Gln Glu Thr Phe Cys Cys Pro Gln Cys Arg Ala Pro

50

55

60

65

ttt cat atg gat agc ctc cga ccc aac aag cag ctg gga agc ctc att 719

Phe His Met Asp Ser Leu Arg Pro Asn Lys Gln Leu Gly Ser Leu Ile

70

75

80

gaa gcc ctc aaa gag acg gat caa gaa atg tca tgt gag gaa cac gga 767

Glu Ala Leu Lys Glu Thr Asp Gln Glu Met Ser Cys Glu Glu His Gly

85

90

95

gag cag ttc cac ctg ttc tgc gaa gac gag ggg cag ctc atc tgc tgg 815

Glu Gln Phe His Leu Phe Cys Glu Asp Glu Gly Gln Leu Ile Cys Trp

100

105

110

cgc tgt gag cgg gca cca cag cac aaa ggg cac acc aca gct ctt gtt 863

Arg Cys Glu Arg Ala Pro Gln His Lys Gly His Thr Thr Ala Leu Val

115

120

125

gaa gac gta tgc cag ggc tac aag gaa aag ctc cag aaa gct gtg aca 911

Glu Asp Val Cys Gln Gly Tyr Lys Glu Lys Leu Gln Lys Ala Val Thr

130

135

140

145

aaa ctg aag caa ctt gaa gac aga tgt acg gag cag aag ctg tcc aca 959

Lys Leu Lys Gln Leu Glu Asp Arg Cys Thr Glu Gln Lys Leu Ser Thr

150

155

160

gca atg cga ata act aaa tgg aaa gag aag gta cag att cag aga caa 1007

Ala Met Arg Ile Thr Lys Trp Lys Glu Lys Val Gln Ile Gln Arg Gln

165

170

175

aaa atc cgg tct gac ttt aag aat ctc cag tgt ttc cta cat gag gaa 1055

Lys Ile Arg Ser Asp Phe Lys Asn Leu Gln Cys Phe Leu His Glu Glu

180

185

190

gag aag tct tat ctc tgg agg ctg gag aaa gaa gaa caa cag act ctg 1103

Glu Lys Ser Tyr Leu Trp Arg Leu Glu Lys Glu Glu Gln Gln Thr Leu

195

200

205

agt aga ctg agg gac tat gag gct ggt ctg ggg ctg aag agc aat gaa 1151

Ser Arg Leu Arg Asp Tyr Glu Ala Gly Leu Gly Leu Lys Ser Asn Glu

210

215

220

225

ctc aag agc cac atc ctg gaa ctg gag gaa aaa tgt cag ggc tca gcc 1199

Leu Lys Ser His Ile Leu Glu Leu Glu Glu Lys Cys Gln Gly Ser Ala

230

235

240

cag aaa ttg ctg cag aat gtg aat gac act ttg agc agg agt tgg gct 1247

Gln Lys Leu Leu Gln Asn Val Asn Asp Thr Leu Ser Arg Ser Trp Ala

245

250

255

gtg aag ctg gaa aca tca gag gct gtc tcc ttg gaa ctt cat act atg 1295

Val Lys Leu Glu Thr Ser Glu Ala Val Ser Leu Glu Leu His Thr Met

260

265

270

tgc aat gtt tcc aag ctt tac ttc gat gtg aag aaa atg tta agg agt 1343

Cys Asn Val Ser Lys Leu Tyr Phe Asp Val Lys Lys Met Leu Arg Ser

275

280

285

cat caa gtt agt gtg act ctg gat cca gat aca gct cat cac gaa cta 1391

His Gln Val Ser Val Thr Leu Asp Pro Asp Thr Ala His His Glu Leu

290 295 300 305

att ctc tct gag gat cgg aga caa gtg act cgt gga tac acc cag gag 1439
Ile Leu Ser Glu Asp Arg Arg Gln Val Thr Arg Gly Tyr Thr Gln Glu
310 315 320

aat cag gac aca tct tcc agg aga ttt act gcc ttc ccc tgt gtc ttg 1487
Asn Gln Asp Thr Ser Ser Arg Arg Phe Thr Ala Phe Pro Cys Val Leu
325 330 335

ggt tgt gaa ggc ttc acc tca gga aga cgt tac ttt gaa gtg gat gtt 1535
Gly Cys Glu Gly Phe Thr Ser Gly Arg Arg Tyr Phe Glu Val Asp Val
340 345 350

ggc gaa gga acc gga tgg gat tta gga gtt tgt atg gaa aat gtg cag 1583
Gly Glu Gly Thr Gly Trp Asp Leu Gly Val Cys Met Glu Asn Val Gln
355 360 365

agg ggc act ggc atg aag caa gag cct cag tct gga ttc tgg acc ctc 1631
Arg Gly Thr Gly Met Lys Gln Glu Pro Gln Ser Gly Phe Trp Thr Leu
370 375 380 385

agg ctg tgc aaa aag aaa ggc tat gta gca ctt act tct ccc cca act 1679
Arg Leu Cys Lys Lys Lys Gly Tyr Val Ala Leu Thr Ser Pro Pro Thr
390 395 400

tcc ctt cat ctg cat gag cag ccc ctg ctt gtg gga att ttt ctg gac 1727
Ser Leu His Leu His Glu Gln Pro Leu Leu Val Gly Ile Phe Leu Asp
405 410 415
349/735

tat gag gcc gga gtt gta tcc ttt tat aac ggg aat act ggc tgc cac 1775
Tyr Glu Ala Gly Val Val Ser Phe Tyr Asn Gly Asn Thr Gly Cys His
420 425 430

atc ttt act ttc ccg aag gct tcc ttc tct gat act ctc egg ccc tat 1823
Ile Phe Thr Phe Pro Lys Ala Ser Phe Ser Asp Thr Leu Arg Pro Tyr
435 440 445

ttc cag gtt tat caa tat tct cct ttg ttt ctg cct ccc cca ggt gac 1871
Phe Gln Val Tyr Gln Tyr Ser Pro Leu Phe Leu Pro Pro Pro Gly Asp
450 455 460 465

taaggaaaag agcagaagct ccttggttta accagcacag agaaaataat ataaatccca 1931

taagggcag 1940

- <210> 101
- <211> 685
- <212> PRT
- <213> Homo sapiens

<400> 101
Met Glu Leu Leu Arg Thr Ile Thr Tyr Gln Pro Ala Ala Ser Thr Lys
1 5 10 15

Met Cys Glu Gln Ala Leu Gly Lys Gly Cys Gly Ala Asp Ser Lys Lys
20 25 30
350/735

Lys Arg Pro Pro Gln Pro Pro Glu Glu Ser Gln Pro Pro Gln Ser Gln
 35 40 45

Ala Gln Val Pro Pro Ala Ala Pro His His His His His His Ser His
 50 55 60

Ser Gly Pro Glu Ile Ser Arg Ile Ile Val Asp Pro Thr Thr Gly Lys
 65 70 75 80

Arg Tyr Cys Arg Gly Lys Val Leu Gly Lys Gly Gly Phe Ala Lys Cys
 85 90 95

Tyr Glu Met Thr Asp Leu Thr Asn Asn Lys Val Tyr Ala Ala Lys Ile
 100 105 110

Ile Pro His Ser Arg Val Ala Lys Pro His Gln Arg Glu Lys Ile Asp
 115 120 125

Lys Glu Ile Glu Leu His Arg Ile Leu His His Lys His Val Val Gln
 130 135 140

Phe Tyr His Tyr Phe Glu Asp Lys Glu Asn Ile Tyr Ile Leu Leu Glu
 145 150 155 160

Tyr Cys Ser Arg Arg Ser Met Ala His Ile Leu Lys Ala Arg Lys Val
 165 170 175

Leu Thr Glu Pro Glu Val Arg Tyr Tyr Leu Arg Gln Ile Val Ser Gly
 351/735

180

185

190

Leu Lys Tyr Leu His Glu Gln Glu Ile Leu His Arg Asp Leu Lys Leu

195

200

205

Gly Asn Phe Phe Ile Asn Glu Ala Met Glu Leu Lys Val Gly Asp Phe

210

215

220

Gly Leu Ala Ala Arg Leu Glu Pro Leu Glu His Arg Arg Arg Thr Ile

225

230

235

240

Cys Gly Thr Pro Asn Tyr Leu Ser Pro Glu Val Leu Asn Lys Gln Gly

245

250

255

His Gly Cys Glu Ser Asp Ile Trp Ala Leu Gly Cys Val Met Tyr Thr

260

265

270

Met Leu Leu Gly Arg Pro Pro Phe Glu Thr Thr Asn Leu Lys Glu Thr

275

280

285

Tyr Arg Cys Ile Arg Glu Ala Arg Tyr Thr Met Pro Ser Ser Leu Leu

290

295

300

Ala Pro Ala Lys His Leu Ile Ala Ser Met Leu Ser Lys Asn Pro Glu

305

310

315

320

Asp Arg Pro Ser Leu Asp Asp Ile Ile Arg His Asp Phe Phe Leu Gln

325

330

335

..

Gly Phe Thr Pro Asp Arg Leu Ser Ser Ser Cys Cys His Thr Val Pro

340

345

350

Asp Phe His Leu Ser Ser Pro Ala Lys Asn Phe Phe Lys Lys Ala Ala

355

360

365

Ala Ala Leu Phe Gly Gly Lys Lys Asp Lys Ala Arg Tyr Ile Asp Thr

370

375

380

His Asn Arg Val Ser Lys Glu Asp Glu Asp Ile Tyr Lys Leu Arg His

385

390

395

400

Asp Leu Lys Lys Thr Ser Ile Thr Gln Gln Pro Ser Lys His Arg Thr

405

410

415

Asp Glu Glu Leu Gln Pro Pro Thr Thr Thr Val Ala Arg Ser Gly Thr

420

425

430

Pro Ala Val Glu Asn Lys Gln Gln Ile Gly Asp Ala Ile Arg Met Ile

435

440

445

Val Arg Gly Thr Leu Gly Ser Cys Ser Ser Ser Ser Glu Cys Leu Glu

450

455

460

Asp Ser Thr Met Gly Ser Val Ala Asp Thr Val Ala Arg Val Leu Arg

465

470

475

480

Gly Cys Leu Glu Asn Met Pro Glu Ala Asp Cys Ile Pro Lys Glu Gln

485

490

495

353/735

.. .. .

Leu Ser Thr Ser Phe Gln Trp Val Thr Lys Trp Val Asp Tyr Ser Asn
500 505 510

Lys Tyr Gly Phe Gly Tyr Gln Leu Ser Asp His Thr Val Gly Val Leu
515 520 525

Phe Asn Asn Gly Ala His Met Ser Leu Leu Pro Asp Lys Lys Thr Val
530 535 540

His Tyr Tyr Ala Glu Leu Gly Gln Cys Ser Val Phe Pro Ala Thr Asp
545 550 555 560

Ala Pro Glu Gln Phe Ile Ser Gln Val Thr Val Leu Lys Tyr Phe Ser
565 570 575

His Tyr Met Glu Glu Asn Leu Met Asp Gly Gly Asp Leu Pro Ser Val
580 585 590

Thr Asp Ile Arg Arg Pro Arg Leu Tyr Leu Leu Gln Trp Leu Lys Ser
595 600 605

Asp Lys Ala Leu Met Met Leu Phe Asn Asp Gly Thr Phe Gln Val Asn
610 615 620

Phe Tyr His Asp His Thr Lys Ile Ile Ile Cys Ser Gln Asn Glu Glu
625 630 635 640

Tyr Leu Leu Thr Tyr Ile Asn Glu Asp Arg Ile Ser Thr Thr Phe Arg
354/735

645 650 655

Leu Thr Thr Leu Leu Met Ser Gly Cys Ser Ser Glu Leu Lys Asn Arg

660 665 670

Met Glu Tyr Ala Leu Asn Met Leu Leu Gln Arg Cys Asn

675 680 685

- <210> 102
- <211> 2783
- <212> DNA
- <213> Homo sapiens

- <220>
- <221> CDS
- <222> (128).. (2182)

<400> 102

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cggccggctc ggacgtgtga ccgcgcctag ggggtggcag cgggcagtcg ggggcggcaa 120

ggcgacc atg gag ctt ttg cgg act atc acc tac cag cca gcc gcc agc 169

Met Glu Leu Leu Arg Thr Ile Thr Tyr Gln Pro Ala Ala Ser

1 5 10

acc aaa atg tgc gag cag gcg ctg ggc aag ggt tgc gga gca gac tcg 217

Thr Lys Met Cys Glu Gln Ala Leu Gly Lys Gly Cys Gly Ala Asp Ser

15 20 25 30

aag aag aag cgg ccg ccg cag ccc ccc gag gaa tcg cag cca cct cag 265
Lys Lys Lys Arg Pro Pro Gln Pro Pro Glu Glu Ser Gln Pro Pro Gln
35 40 45

tcc cag gcg caa gtg ccc ccg gcg gcc cct cac cac cat cac cac cat 313
Ser Gln Ala Gln Val Pro Pro Ala Ala Pro His His His His His His
505560

tcg cac tcg ggg cgg gag atc tcg cgg att atc gtc gac ccc acg act 361
Ser His Ser Gly Pro Glu Ile Ser Arg Ile Ile Val Asp Pro Thr Thr
65 70 75

ggg aag cgc tac tgc cgg ggc aaa gtg ctg gga aag ggt ggc ttt gca 409
Gly Lys Arg Tyr Cys Arg Gly Lys Val Leu Gly Lys Gly Gly Phe Ala
80 85 90

aaa tgt tac gag atg aca gat ttg aca aat aac aaa gtc tac gcc gca 457
Lys Cys Tyr Glu Met Thr Asp Leu Thr Asn Asn Lys Val Tyr Ala Ala
95 100 105 110

aaa att att cct cac agc aga gta gct aaa cct cat caa agg gaa aag 505
Lys Ile Ile Pro His Ser Arg Val Ala Lys Pro His Gln Arg Glu Lys
115 120 125

att gac aaa gaa ata gag ctt cac aga att ctt cat cat aag cat gta 553
Ile Asp Lys Glu Ile Glu Leu His Arg Ile Leu His His Lys His Val
130 135 140

gtg cag ttt tac cac tac ttc gag gac aaa gaa aac att tac att ctc 601

Val Gln Phe Tyr His Tyr Phe Glu Asp Lys Glu Asn Ile Tyr Ile Leu

145

150

155

ttg gaa tac tgc agt aga agg tca atg gct cat att ttg aaa gca aga 649

Leu Glu Tyr Cys Ser Arg Arg Ser Met Ala His Ile Leu Lys Ala Arg

160

165

170

aag gtg ttg aca gag cca gaa gtt cga tac tac ctc agg cag att gtg 697

Lys Val Leu Thr Glu Pro Glu Val Arg Tyr Tyr Leu Arg Gln Ile Val

175

180

185

190

tct gga ctg aaa tac ctt cat gaa caa gaa atc ttg cac aga gat ctc 745

Ser Gly Leu Lys Tyr Leu His Glu Gln Glu Ile Leu His Arg Asp Leu

195

200

205

aaa cta ggg aac ttt ttt att aat gaa gcc atg gaa cta aaa gtt ggg 793

Lys Leu Gly Asn Phe Phe Ile Asn Glu Ala Met Glu Leu Lys Val Gly

210

215

220

gac ttc ggt ctg gca gcc agg cta gaa ccc ttg gaa cac aga agg aga 841

Asp Phe Gly Leu Ala Ala Arg Leu Glu Pro Leu Glu His Arg Arg Arg

225

230

235

acg ata tgt ggt acc cca aat tat ctc tct cct gaa gtc ctc aac aaa 889

Thr Ile Cys Gly Thr Pro Asn Tyr Leu Ser Pro Glu Val Leu Asn Lys

240

245

250

caa gga cat ggc tgt gaa tca gac att tgg gcc ctg ggc tgt gta atg 937
Gln Gly His Gly Cys Glu Ser Asp Ile Trp Ala Leu Gly Cys Val Met
255 260 265 270

tat aca atg tta cta ggg agg ccc cca ttt gaa act aca aat ctc aaa 985
Tyr Thr Met Leu Leu Gly Arg Pro Pro Phe Glu Thr Thr Asn Leu Lys
275 280 285

gaa act tat agg tgc ata agg gaa gca agg tat aca atg ccg tcc tca 1033
Glu Thr Tyr Arg Cys Ile Arg Glu Ala Arg Tyr Thr Met Pro Ser Ser
290 295 300

ttg ctg gct cct gcc aag cac tta att gct agt atg ttg tcc aaa aac 1081
Leu Leu Ala Pro Ala Lys His Leu Ile Ala Ser Met Leu Ser Lys Asn
305 310 315

cca gag gat cgt ccc agt ttg gat gac atc att cga cat gac' ttt ttt 1129
Pro Glu Asp Arg Pro Ser Leu Asp Asp Ile Ile Arg His Asp Phe Phe
320 325 330

ttg cag ggc ttc act ccg gac aga ctg tct tct agc tgt tgt cat aca 1177
Leu Gln Gly Phe Thr Pro Asp Arg Leu Ser Ser Ser Cys Cys His Thr
335 340 345 350

gtt cca gat ttc cac tta tca agc cca gct aag aat ttc ttt aag aaa 1225
Val Pro Asp Phe His Leu Ser Ser Pro Ala Lys Asn Phe Phe Lys Lys
355 360 365

gca gct gct gct ctt ttt ggt ggc aaa aaa gac aaa gca aga tat att 1273
358/735

Ala Ala Ala Ala Leu Phe Gly Gly Lys Lys Asp Lys Ala Arg Tyr Ile

370

375

380

gac aca cat aat aga gtg tct aaa gaa gat gaa gac atc tac aag ctt 1321

Asp Thr His Asn Arg Val Ser Lys Glu Asp Glu Asp Ile Tyr Lys Leu

385

390

395

agg cat gat ttg aaa aag act tca ata act cag caa ccc agc aaa cac 1369

Arg His Asp Leu Lys Lys Thr Ser Ile Thr Gln Gln Pro Ser Lys His

400

405

410

agg aca gat gag gag ctc cag cca cct acc acc aca gtt gcc agg tct 1417

Arg Thr Asp Glu Glu Leu Gln Pro Pro Thr Thr Thr Val Ala Arg Ser

415

420

425

430

gga aca ccc gca gta gaa aac aag cag cag att ggg gat gct att cgg 1465

Gly Thr Pro Ala Val Glu Asn Lys Gln Gln Ile Gly Asp Ala Ile Arg

435

440

445

atg ata gtc aga ggg act ctt ggc agc tgt agc agc agc agt gaa tgc 1513

Met Ile Val Arg Gly Thr Leu Gly Ser Cys Ser Ser Ser Ser Glu Cys

450

455

460

ctt gaa gac agt acc atg gga agt gtt gca gac aca gtg gca agg gtt 1561

Leu Glu Asp Ser Thr Met Gly Ser Val Ala Asp Thr Val Ala Arg Val

465

470

475

ctt cgg gga tgt ctg gaa aac atg ccg gaa gct gat tgc att ccc aaa 1609

Leu Arg Gly Cys Leu Glu Asn Met Pro Glu Ala Asp Cys Ile Pro Lys

480

485

490

gag cag ctg agc aca tca ttt cag tgg gtc acc aaa tgg gtt gat tac 1657

Glu Gln Leu Ser Thr Ser Phe Gln Trp Val Thr Lys Trp Val Asp Tyr

495

500

505

510

tct aac aaa tat ggc ttt ggg tac cag ctc tca gac cac acc gtc ggt 1705

Ser Asn Lys Tyr Gly Phe Gly Tyr Gln Leu Ser Asp His Thr Val Gly

515

520

525

gtc ctt ttc aac aat ggt gct cac atg agc ctc ctt cca gac aaa aaa 1753

Val Leu Phe Asn Asn Gly Ala His Met Ser Leu Leu Pro Asp Lys Lys

530

535

540

aca gtt cac tat tac gca gag ctt ggc caa tgc tca gtt ttc cca gca 1801

Thr Val His Tyr Tyr Ala Glu Leu Gly Gln Cys Ser Val Phe Pro Ala

545

550

555

aca gat gct cct gag caa ttt att agt caa gtg acg gtg ctg aaa tac 1849

Thr Asp Ala Pro Glu Gln Phe Ile Ser Gln Val Thr Val Leu Lys Tyr

560

565

570

ttt tct cat tac atg gag gag aac ctc atg gat ggt gga gat ctg cct 1897

Phe Ser His Tyr Met Glu Glu Asn Leu Met Asp Gly Gly Asp Leu Pro

575

580

585

590

agt gtt act gat att cga aga cct cgg ctc tac ctc ctt cag tgg cta 1945

Ser Val Thr Asp Ile Arg Arg Pro Arg Leu Tyr Leu Leu Gln Trp Leu

595

600

605

aaa tct gat aag gcc cta atg atg ctc ttt aat gat ggc acc ttt cag 1993

Lys Ser Asp Lys Ala Leu Met Met Leu Phe Asn Asp Gly Thr Phe Gln

610

615

620

gtg aat ttc tac cat gat cat aca aaa atc atc atc tgt agc caa aat 2041

Val Asn Phe Tyr His Asp His Thr Lys Ile Ile Ile Cys Ser Gln Asn

625

630

635

gaa gaa tac ctt ctc acc tac atc aat gag gat agg ata tct aca act 2089

Glu Glu Tyr Leu Leu Thr Tyr Ile Asn Glu Asp Arg Ile Ser Thr Thr

640

645

650

ttc agg ctg aca act ctg ctg atg tct ggc tgt tca tca gaa tta aaa 2137

Phe Arg Leu Thr Thr Leu Leu Met Ser Gly Cys Ser Ser Glu Leu Lys

655

660

665

670

aat cga atg gaa tat gcc ctg aac atg ctc tta caa aga tgt aac 2182

Asn Arg Met Glu Tyr Ala Leu Asn Met Leu Leu Gln Arg Cys Asn

675

680

685

tgaaagactt ttcgatgga ccctatggga ctctctttt ccactgtgag atctacaggg 2242

aacccaaaag aatgatctag agtatgttga agaagatgga catgtggtgg tacgaaaaca 2302

attcccctgt ggccctgctgg actgggtgga accagaacag gctaaggcat acagttcttg 2362

actttggaca atccaagagt gaaccagaat gcagttttcc ttgagatacc tgttttaaaa 2422

ggtttttcag acaattttgc agaaaggtgc attgattcct aaattctctc tgttgagagc 2482

atttcagcca gaggactttg gaactgtgaa tatacttcct gaaggggagg gagaagggag 2542

gaagctccca tgttgtttaa aggctgtaat tggagcagct tttggctgcg taactgtgaa 2602

ctatggccat atataatfff ttttcattaa tttttgaaga tacttgtggc tggaaaagtg 2662

cattccttgt taataaactt tttatttatt acageccaaa gagcagtatt tattatcaaa 2722

atgtcttttt ttttatgttg accattttaa accgttggca ataaagagta tgaaaacgca 2782

g 2783

<210> 103

<211> 161

<212> PRT

<213> Homo sapiens

<400> 103

Met Ser Val Pro Gly Pro Tyr Gln Ala Ala Thr Gly Pro Ser Ser Ala

1 5 10 15

Pro Ser Ala Pro Pro Ser Tyr Glu Glu Thr Val Ala Val Asn Ser Tyr

20 25 30

Tyr Pro Thr Pro Pro Ala Pro Met Pro Gly Pro Thr Thr Gly Leu Val

35 40 45

Thr Gly Pro Asp Gly Lys Gly Met Asn Pro Pro Ser Tyr Tyr Thr Gln
50 55 60

Pro Ala Pro Ile Pro Asn Asn Asn Pro Ile Thr Val Gln Thr Val Tyr
65 70 75 80

Val Gln His Pro Ile Thr Phe Leu Asp Arg Pro Ile Gln Met Cys Cys
85 90 95

Pro Ser Cys Asn Lys Met Ile Val Ser Gln Leu Ser Tyr Asn Ala Gly
100 105 110

Ala Leu Thr Trp Leu Ser Cys Gly Ser Leu Cys Leu Leu Gly Cys Ile
115 120 125

Ala Gly Cys Cys Phe Ile Pro Phe Cys Val Asp Ala Leu Gln Asp Val
130 135 140

Asp His Tyr Cys Pro Asn Cys Arg Ala Leu Leu Gly Thr Tyr Lys Arg
145 150 155 160

Leu

<210> 104

<211> 1589

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (70).. (552)

<400> 104

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ggcggtaaaa atg tcg gtt cca gga cct tac cag gcg gcc act ggg cct tcc 111

Met Ser Val Pro Gly Pro Tyr Gln Ala Ala Thr Gly Pro Ser

1 5 10

tea gca cca tcc gca cct cca tcc tat gaa gag aca gtg gct gtt aac 159

Ser Ala Pro Ser Ala Pro Pro Ser Tyr Glu Glu Thr Val Ala Val Asn

15 20 25 30

agt tat tac ccc aca cct cca gct ccc atg cct ggg cca act acg ggg 207

Ser Tyr Tyr Pro Thr Pro Pro Ala Pro Met Pro Gly Pro Thr Thr Gly

35 40 45

ctt gtg acg ggg cct gat ggg aag ggc atg aat cct cct tcg tat tat 255

Leu Val Thr Gly Pro Asp Gly Lys Gly Met Asn Pro Pro Ser Tyr Tyr

50 55 60

acc cag cca gcg ccc atc ccc aat aac aat cca att acc gtg cag acg 303

Thr Gln Pro Ala Pro Ile Pro Asn Asn Asn Pro Ile Thr Val Gln Thr

65 70 75

gtc tac gtg cag cac ccc atc acc ttt ttg gac cgc cct atc caa atg 351

Val Tyr Val Gln His Pro Ile Thr Phe Leu Asp Arg Pro Ile Gln Met

80

85

90

tgt tgt cct tcc tgc aac aag atg atc gtg agt cag ctg tcc tat aac 399

Cys Cys Pro Ser Cys Asn Lys Met Ile Val Ser Gln Leu Ser Tyr Asn

95

100

105

110

gcc ggt gct ctg acc tgg ctg tcc tgc ggg agc ctg tgc ctg ctg ggg 447

Ala Gly Ala Leu Thr Trp Leu Ser Cys Gly Ser Leu Cys Leu Leu Gly

115

120

125

tgc ata gcg ggc tgc tgc ttc atc ccc ttc tgc gtg gat gcc ctg cag 495

Cys Ile Ala Gly Cys Cys Phe Ile Pro Phe Cys Val Asp Ala Leu Gln

130

135

140

gac gtg gac cat tac tgt ccc aac tgc aga gct ctc ctg ggc acc tac 543

Asp Val Asp His Tyr Cys Pro Asn Cys Arg Ala Leu Leu Gly Thr Tyr

145

150

155

aag cgt ttg taggactcag ccagacgtgg agggagccgg gtgccgcagg 592

Lys Arg Leu

160

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tgggcctgaa cataatttca agaggaggat ttataaaacc attttctgta atcaaatgat 1552

tggtgtcatt ttcccatttg ccaatgtagt ctcactt 1589

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atgcatgcta gaaaaatagg gctggatctt atcactgccc tgtctcccct tgttttctctg 1252

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Leu Asp Pro Pro Thr Asp Leu Lys Phe Lys Gly Pro Phe Thr Asp Val

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25

30

Val Thr Thr Asn Leu Lys Leu Arg Asn Pro Ser Asp Arg Lys Val Cys

35

40

45

Phe Lys Val Lys Thr Thr Ala Pro Arg Arg Tyr Cys Val Arg Pro Asn

50

55

60

Ser Gly Ile Ile Asp Pro Gly Ser Thr Val Thr Val Ser Val Met Leu

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70

75

80

Gln Pro Phe Asp Tyr Asp Pro Asn Glu Lys Ser Lys His Lys Phe Met

85

90

95

Val Gln Thr Ile Phe Ala Pro Pro Asn Thr Ser Asp Met Glu Ala Val

100

105

110

Trp Lys Glu Ala Lys Pro Asp Glu Leu Met Asp Ser Lys Leu Arg Cys

115

120

125

Val Phe Glu Met Pro Asn Glu Asn Asp Lys Leu Asn Asp Met Glu Pro

130

135

140

Ser Lys Ala Val Pro Leu Asn Ala Ser Lys Gln Asp Gly Pro Met Pro

145

150

155

160

Lys Pro His Ser Val Ser Leu Asn Asp Thr Glu Thr Arg Lys Leu Met

165

170

175

Glu Glu Cys Lys Arg Leu Gln Gly Glu Met Met Lys Leu Ser Glu Glu

180

185

190

Asn Arg His Leu Arg Asp Glu Gly Leu Arg Leu Arg Lys Val Ala His

195

200

205

Ser Asp Lys Pro Gly Ser Thr Ser Thr Ala Ser Phe Arg Asp Asn Val

210

215

220

Thr Ser Pro Leu Pro Ser Leu Leu Val Val Ile Ala Ala Ile Phe Ile

225

230

235

240

Gly Phe Phe Leu Gly Lys Phe Ile Leu

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<212> DNA

<213> Homo sapiens

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<222> (232).. (978)

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gaccagcgg gtggcccacc gaaccgtga cacagcggca ggcgttaggg ctcgggagcc 120

gcgagcctgg cctcgtccta gagtcggcc gagecgtcgc cgccgtcgtc ccccgcccc 180

agtcagcaaa ccgcgcgcgc gggcgcgcgc ccgctctgeg ctgtctctcc g atg gcg 237

Met Ala

1

tcc gcc tca ggg gcc atg gcg aag cac gag cag atc ctg gtc etc gat 285

Ser Ala Ser Gly Ala Met Ala Lys His Glu Gln Ile Leu Val Leu Asp

5

10

15

cgc gcc aca gac ctc aaa ttc aaa ggc ccc ttc aca gat gta gtc act 333

Pro Pro Thr Asp Leu Lys Phe Lys Gly Pro Phe Thr Asp Val Val Thr

20

25

30

aca aat ctt aaa ttg cga aat cca tcg gat aga aaa gtg tgt ttc aaa 381

Thr Asn Leu Lys Leu Arg Asn Pro Ser Asp Arg Lys Val Cys Phe Lys

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40

45

50

gtg aag act aca gca cct cgc cgg tac tgt gtg agg ccc aac agt gga 429

Val Lys Thr Thr Ala Pro Arg Arg Tyr Cys Val Arg Pro Asn Ser Gly

55

60

65

att att gac cca ggg tca act gtg act gtt tca gta atg cta cag ccc 477

Ile Ile Asp Pro Gly Ser Thr Val Thr Val Ser Val Met Leu Gln Pro

70

75

80

ttt gac tat gat ccg aat gaa aag agt aaa cac aag ttt atg gta cag 525

Phe Asp Tyr Asp Pro Asn Glu Lys Ser Lys His Lys Phe Met Val Gln

85

90

95

aca att ttt gct cca cca aac act tca gat atg gaa gct gtg tgg aaa 573

215

220

225

cct ctt cct tca ctt ctt gtt gta att gca gcc att ttc att gga ttc 957
Pro Leu Pro Ser Leu Leu Val Val Ile Ala Ala Ile Phe Ile Gly Phe

230

235

240

ttt cta ggg aaa ttc atc ttg tagagtgaag catgcagagt gctgtttctt 1008
Phe Leu Gly Lys Phe Ile Leu

245

tttttttttt tctcttgacc agaaaaagat ttgtttacct accatttcat tggtagtatg 1068

gcccacgggtg accatttttt tgtgtgtaca gcgtcatata ggctttgcct ttaatgatct 1128

cttacggtta gaaaacacaa taaaaacaaa ctgttcggct actggacagg ttgtatatta 1188

ccagatcatc actagcagat gtcagttgca cattgagtc tttatgaaat tcataaataa 1248

agaattgttc tttctttgtg gttttaataa gagttcaaga attgttcaga gtcttgtaaa 1308

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tgcctcttac agtgtaaatt tttcctcctt tacctttgct aatatcatgg cagaattttt 1488

cttatccctt gtgaggcagt tgttgactga gtttttcate cttaaatcc tgtcccatgg 1548

tatttaacat aaaaaaaaaat aaaactgtta acagattcctt gctcgat 1595

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Ala Ser Ala Ala Ser Glu Gly Gly Phe Thr Ala Thr Gly Gln Arg Gln

20 25 30

Leu Arg Pro Glu His Phe Gln Glu Val Gly Tyr Ala Ala Pro Pro Ser

35 40 45

Pro Pro Leu Ser Arg Ser Leu Pro Met Asp His Pro Asp Ser Ser Gln

50 55 60

His Gly Pro Pro Phe Glu Gly Gln Ser Gln Val Gln Pro Pro Pro Ser

65 70 75 80

Gln Glu Ala Thr Pro Leu Gln Gln Glu Lys Leu Leu Pro Ala Gln Leu

85 90 95

Pro Ala Glu Lys Glu Val Gly Pro Pro Leu Pro Gln Glu Ala Val Pro

100 105 110

Leu Gln Lys Glu Leu Pro Ser Leu Gln His Pro Asn Glu Gln Lys Glu

115

120

125

Gly Thr Pro Ala Pro Phe Gly Asp Gln Ser His Pro Glu Pro Glu Ser

130

135

140

Trp Asn Ala Ala Gln His Cys Gln Gln Asp Arg Ser Gln Gly Gly Trp

145

150

155

160

Gly His Arg Leu Asp Gly Phe Pro Pro Gly Arg Pro Ser Pro Asp Asn

165

170

175

Leu Asn Gln Ile Cys Leu Pro Asn Arg Gln His Val Val Tyr Gly Pro

180

185

190

Trp Asn Leu Pro Gln Ser Ser Tyr Ser His Leu Thr Arg Gln Gly Glu

195

200

205

Thr Leu Asn Phe Leu Glu Ile Gly Tyr Ser Arg Cys Cys His Cys Arg

210

215

220

Ser His Thr Asn Arg Leu Glu Cys Ala Lys Leu Val Trp Glu Glu Ala

225

230

235

240

Met Ser Arg Phe Cys Glu Ala Glu Phe Ser Val Lys Thr Arg Pro His

245

250

255

Trp Cys Cys Thr Arg Gln Gly Glu Ala Arg Phe Ser Cys Phe Gln Glu

260

265

270

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Glu Ala Pro Gln Pro His Tyr Gln Leu Arg Ala Cys Pro Ser His Gln

275

280

285

Pro Asp Ile Ser Ser Gly Leu Glu Leu Pro Phe Pro Pro Gly Val Pro

290

295

300

Thr Leu Asp Asn Ile Lys Asn Ile Cys His Leu Arg Arg Phe Arg Ser

305

310

315

320

Val Pro Arg Asn Leu Pro Ala Thr Asp Pro Leu Gln Arg Glu Leu Leu

325

330

335

Ala Leu Ile Gln Leu Glu Arg Glu Phe Gln Arg Cys Cys Arg Gln Gly

340

345

350

Asn Asn His Thr Cys Thr Trp Lys Ala Trp Glu Asp Thr Leu Asp Lys

355

360

365

Tyr Cys Asp Arg Glu Tyr Ala Val Lys Thr His His His Leu Cys Cys

370

375

380

Arg His Pro Pro Ser Pro Thr Arg Asp Glu Cys Phe Ala Arg Arg Ala

385

390

395

400

Pro Tyr Pro Asn Tyr Asp Arg Asp Ile Leu Thr Ile Asp Ile Gly Arg

405

410

415

Val Thr Pro Asn Leu Met Gly His Leu Cys Gly Asn Gln Arg Val Leu

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420

425

430

Thr Lys His Lys His Ile Pro Gly Leu Ile His Asn Met Thr Ala Arg

435

440

445

Cys Cys Asp Leu Pro Phe Pro Glu Gln Ala Cys Cys Ala Glu Glu Glu

450

455

460

Lys Leu Thr Phe Ile Asn Asp Leu Cys Gly Pro Arg Arg Asn Ile Trp

465

470

475

480

Arg Asp Pro Ala Leu Cys Cys Tyr Leu Ser Pro Gly Asp Glu Gln Val

485

490

495

Asn Cys Phe Asn Ile Asn Tyr Leu Arg Asn Val Ala Leu Val Ser Gly

500

505

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Asp Thr Glu Asn Ala Lys Gly Gln Gly Glu Gln Gly Ser Thr Gly Gly

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520

525

Thr Asn Ile Ser Ser Thr Ser Glu Pro Lys Glu Glu

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535

540

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<211> 1810

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<213> Homo sapiens

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<222> (102).. (1721)

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Met Gly Thr Thr Ala

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5

aga gca gcc ttg gtc ttg acc tat ttg gct gtt gct tct gct gcc tct 164

Arg Ala Ala Leu Val Leu Thr Tyr Leu Ala Val Ala Ser Ala Ala Ser

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15

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gag gga ggc ttc acg gct aca gga cag agg cag ctg agg cca gag cac 212

Glu Gly Gly Phe Thr Ala Thr Gly Gln Arg Gln Leu Arg Pro Glu His

25

30

35

ttt caa gaa gtt ggc tac gca gct ccc ccc tcc cca ccc cta tcc cga 260

Phe Gln Glu Val Gly Tyr Ala Ala Pro Pro Ser Pro Pro Leu Ser Arg

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45

50

agc ctc ccc atg gat cac cct gac tcc tct cag cat ggc cct ccc ttt 308

Ser Leu Pro Met Asp His Pro Asp Ser Ser Gln His Gly Pro Pro Phe

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gag gga cag agt caa gtg cag ccc cct ccc tct cag gag gcc acc cct 356

Glu Gly Gln Ser Gln Val Gln Pro Pro Pro Ser Gln Glu Ala Thr Pro

381/735

70

75

80

85

ctc caa cag gaa aag ctg cta cct gcc caa ctc cct gct gaa aag gaa 404

Leu Gln Gln Glu Lys Leu Leu Pro Ala Gln Leu Pro Ala Glu Lys Glu

90

95

100

gtg ggt ccc cct ctc cct cag gaa gct gtc ccc ctc caa aaa gag ctg 452

Val Gly Pro Pro Leu Pro Gln Glu Ala Val Pro Leu Gln Lys Glu Leu

105

110

115

ccc tct ctc cag cac ccc aat gaa cag aag gaa gga acg cca gct cca 500

Pro Ser Leu Gln His Pro Asn Glu Gln Lys Glu Gly Thr Pro Ala Pro

120

125

130

ttt ggg gac cag agc cat cca gaa cct gag tcc tgg aat gca gcc cag 548

Phe Gly Asp Gln Ser His Pro Glu Pro Glu Ser Trp Asn Ala Ala Gln

135

140

145

cac tgc caa cag gac cgg tcc caa ggg ggc tgg ggc cac cgg ctg gat 596

His Cys Gln Gln Asp Arg Ser Gln Gly Gly Trp Gly His Arg Leu Asp

150

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160

165

ggc ttc ccc cct ggg cgg cct tct cca gac aat ctg aac caa atc tgc 644

Gly Phe Pro Pro Gly Arg Pro Ser Pro Asp Asn Leu Asn Gln Ile Cys

170

175

180

ctt cct aac cgt cag cat gtg gta tat ggt ccc tgg aac cta cca cag 692

Leu Pro Asn Arg Gln His Val Val Tyr Gly Pro Trp Asn Leu Pro Gln

185

190

195

tcc agc tac tcc cac ctc act cgc cag ggt gag acc ctc aat ttc ctg 740

Ser Ser Tyr Ser His Leu Thr Arg Gln Gly Glu Thr Leu Asn Phe Leu

200

205

210

gag att gga tat tcc cgc tgc tgc cac tgc cgc agc cac aca aac cgc 788

Glu Ile Gly Tyr Ser Arg Cys Cys His Cys Arg Ser His Thr Asn Arg

215

220

225

cta gag tgt gcc aaa ctt gtg tgg gag gaa gca atg agc cga ttc tgt 836

Leu Glu Cys Ala Lys Leu Val Trp Glu Glu Ala Met Ser Arg Phe Cys

230

235

240

245

gag gcc gag ttc tcg gtc aag acc cga ccc cac tgg tgc tgc acg cgg 884

Glu Ala Glu Phe Ser Val Lys Thr Arg Pro His Trp Cys Cys Thr Arg

250

255

260

cag ggg gag gct cgg ttc tcc tgc ttc cag gag gaa gct ccc cag cca 932

Gln Gly Glu Ala Arg Phe Ser Cys Phe Gln Glu Glu Ala Pro Gln Pro

265

270

275

cac tac cag ctc cgg gcc tgc ccc agc cat cag cct gat att tcc tcg 980

His Tyr Gln Leu Arg Ala Cys Pro Ser His Gln Pro Asp Ile Ser Ser

280

285

290

ggt ctt gag ctg cct ttc cct cct ggg gtg ccc aca ttg gac aat atc 1028

Gly Leu Glu Leu Pro Phe Pro Pro Gly Val Pro Thr Leu Asp Asn Ile

295

300

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aag aac atc tgc cac ctg agg cgc ttc cgc tct gtg cca cgc aac ctg 1076

Lys Asn Ile Cys His Leu Arg Arg Phe Arg Ser Val Pro Arg Asn Leu

310 315 320 325

cca gct act gac ccc cta caa agg gag ctg ctg gca ctg atc cag ctg 1124

Pro Ala Thr Asp Pro Leu Gln Arg Glu Leu Leu Ala Leu Ile Gln Leu

330 335 340

gag agg gag ttc cag cgc tgc tgc cgc cag ggg aac aat cac acc tgt 1172

Glu Arg Glu Phe Gln Arg Cys Cys Arg Gln Gly Asn Asn His Thr Cys

345 350 355

aca tgg aag gcc tgg gag gat acc ctt gac aaa tac tgt gac cgg gag 1220

Thr Trp Lys Ala Trp Glu Asp Thr Leu Asp Lys Tyr Cys Asp Arg Glu

360 365 370

tat gct gtg aag acc cac cac cac ttg tgt tgc cgc cac cct ccc agc 1268

Tyr Ala Val Lys Thr His His His Leu Cys Cys Arg His Pro Pro Ser

375 380 385

cct act cgg gat gag tgc ttt gcc cgt cgg gct cct tac ccc aac tat 1316

Pro Thr Arg Asp Glu Cys Phe Ala Arg Arg Ala Pro Tyr Pro Asn Tyr

390 395 400 405

gac cgg gac atc ttg acc att gac atc ggt cga gtc acc ccc aac ctc 1364

Asp Arg Asp Ile Leu Thr Ile Asp Ile Gly Arg Val Thr Pro Asn Leu

410 415 420

atg ggc cac ctc tgt gga aac caa aga gtt ctc acc aag cat aaa cat 1412

Met Gly His Leu Cys Gly Asn Gln Arg Val Leu Thr Lys His Lys His

425

430

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att cct ggg ctg atc cac aac atg act gcc cgc tgc tgt gac ctg cca 1460

Ile Pro Gly Leu Ile His Asn Met Thr Ala Arg Cys Cys Asp Leu Pro

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445

450

ttt cca gaa cag gcc tgc tgt gca gag gag gag aaa tta acc ttc atc 1508

Phe Pro Glu Gln Ala Cys Cys Ala Glu Glu Glu Lys Leu Thr Phe Ile

455

460

465

aat gat ctg tgt ggt ccc cga cgt aac atc tgg cga gac cct gcc etc 1556

Asn Asp Leu Cys Gly Pro Arg Arg Asn Ile Trp Arg Asp Pro Ala Leu

470

475

480

485

tgc tgt tac ctg agt cct ggg gat gaa cag gtc aac tgc ttc aac atc 1604

Cys Cys Tyr Leu Ser Pro Gly Asp Glu Gln Val Asn Cys Phe Asn Ile

490

495

500

aat tat ctg agg aac gtg gct cta gtg tct gga gac act gag aac gcc 1652

Asn Tyr Leu Arg Asn Val Ala Leu Val Ser Gly Asp Thr Glu Asn Ala

505

510

515

aag ggc cag ggg gag cag ggc tca act gga gga aca aat atc agc tcc 1700

Lys Gly Gln Gly Glu Gln Gly Ser Thr Gly Gly Thr Asn Ile Ser Ser

520

525

530

acc tct gag ccc aag gaa gaa tgagtcaccc cagagcccta gagggtcaga 1751

Thr Ser Glu Pro Lys Glu Glu

Pro Ala Glu Lys Glu Val Gly Pro Pro Leu Pro Gln Glu Ala Val Pro
 100 105 110

Leu Gln Lys Glu Leu Pro Ser Leu Gln His Pro Asn Glu Gln Lys Glu
 115 120 125

Gly Thr Pro Ala Pro Phe Gly Asp Gln Ser His Pro Glu Pro Glu Ser
 130 135 140

Trp Asn Ala Ala Gln His Cys Gln Gln Asp Arg Ser Gln Gly Gly Trp
 145 150 155 160

Gly His Arg Leu Asp Gly Phe Pro Pro Gly Arg Pro Ser Pro Asp Asn
 165 170 175

Leu Asn Gln Ile Cys Leu Pro Asn Arg Gln His Val Val Tyr Gly Pro
 180 185 190

Trp Asn Leu Pro Gln Ser Ser Tyr Ser His Leu Thr Arg Gln Gly Glu
 195 200 205

Thr Leu Asn Phe Leu Glu Ile Gly Tyr Ser Arg Cys Cys His Cys Arg
 210 215 220

Ser His Thr Asn Arg Leu Glu Cys Ala Lys Leu Val Trp Glu Glu Ala
 225 230 235 240

Met Ser Arg Phe Cys Glu Ala Glu Phe Ser Val Lys Thr Arg Pro His
 245 250 255

Trp Cys Cys Thr Arg Gln Gly Glu Ala Arg Phe Ser Cys Phe Gln Glu
260 265 270

Glu Ala Pro Gln Pro His Tyr Gln Leu Arg Ala Cys Pro Ser His Gln
275 280 285

Pro Asp Ile Ser Ser Gly Leu Glu Leu Pro Phe Pro Pro Gly Val Pro
290 295 300

Thr Leu Asp Asn Ile Lys Asn Ile Cys His Leu Arg Arg Phe Arg Ser
305 310 315 320

Val Pro Arg Asn Leu Pro Ala Thr Asp Pro Leu Gln Arg Glu Leu Leu
325 330 335

Ala Leu Ile Gln Leu Glu Arg Glu Phe Gln Arg Cys Cys Arg Gln Gly
340 345 350

Asn Asn His Thr Cys Thr Trp Lys Ala Trp Glu Asp Thr Leu Asp Lys
355 360 365

Tyr Cys Asp Arg Glu Tyr Ala Val Lys Thr His His His Leu Cys Cys
370 375 380

Arg His Pro Pro Ser Pro Thr Arg Asp Glu Cys Phe Ala Arg Arg Ala
385 390 395 400

Pro Tyr Pro Asn Tyr Asp Arg Asp Ile Leu Thr Ile Asp Ile Ser Arg
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all amino acids are present in the protein

405

410

415

Val Thr Pro Asn Leu Met Gly His Leu Cys Gly Asn Gln Arg Val Leu

420

425

430

Thr Lys His Lys His Ile Pro Gly Leu Ile His Asn Met Thr Ala Arg

435

440

445

Cys Cys Asp Leu Pro Phe Pro Glu Gln Ala Cys Cys Ala Glu Glu Glu

450

455

460

Lys Leu Thr Phe Ile Asn Asp Leu Cys Gly Pro Arg Arg Asn Ile Trp

465

470

475

480

Arg Asp Pro Ala Leu Cys Cys Tyr Leu Ser Pro Gly Asp Glu Gln Val

485

490

495

Asn Cys Phe Asn Ile Asn Tyr Leu Arg Asn Val Ala Leu Val Ser Gly

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Asp Thr Glu Asn Ala Lys Gly Gln Gly Glu Gln Gly Ser Thr Gly Gly

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525

Thr Asn Ile Ser Ser Thr Ser Glu Pro Lys Glu Glu

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535

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<210> 112

<211> 1810

<212> DNA

<213> Homo sapiens

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Met Gly Thr Thr Ala

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aga gca gcc ttg gtc ttg acc tat ttg gct gtt gct tct gct gcc tct 164

Arg Ala Ala Leu Val Leu Thr Tyr Leu Ala Val Ala Ser Ala Ala Ser

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gag gga ggc ttc acg gct aca gga cag agg cag ctg agg cca gag cac 212

Glu Gly Gly Phe Thr Ala Thr Gly Gln Arg Gln Leu Arg Pro Glu His

25

30

35

ttt caa gaa gtt ggc tac gca gct ccc ccc tcc cca ccc cta tcc cga 260

Phe Gln Glu Val Gly Tyr Ala Ala Pro Pro Ser Pro Pro Leu Ser Arg

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agc ctc ccc atg gat cac cct gac tcc tct cag cat ggc cct ccc ttt 308

Ser Leu Pro Met Asp His Pro Asp Ser Ser Gln His Gly Pro Pro Phe

55

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gag gga cag agt caa gtg cag ccc cct ccc tct cag gag gcc acc cct 356

Glu Gly Gln Ser Gln Val Gln Pro Pro Pro Ser Gln Glu Ala Thr Pro

70

75

80

85

ctc caa cag gaa aag ctg cta cct gcc caa ctc cct gct gaa aag gaa 404

Leu Gln Gln Glu Lys Leu Leu Pro Ala Gln Leu Pro Ala Glu Lys Glu

90

95

100

gtg ggt ccc cct ctc cct cag gaa gct gtc ccc ctc caa aaa gag ctg 452

Val Gly Pro Pro Leu Pro Gln Glu Ala Val Pro Leu Gln Lys Glu Leu

105

110

115

ccc tct ctc cag cac ccc aat gaa cag aag gaa gga acg cca gct cca 500

Pro Ser Leu Gln His Pro Asn Glu Gln Lys Glu Gly Thr Pro Ala Pro

120

125

130

ttt ggg gac cag agc cat cca gaa cct gag tcc tgg aat gca gcc cag 548

Phe Gly Asp Gln Ser His Pro Glu Pro Glu Ser Trp Asn Ala Ala Gln

135

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145

cac tgc caa cag gac cgg tcc caa ggg ggc tgg ggc cac cgg ctg gat 596

His Cys Gln Gln Asp Arg Ser Gln Gly Gly Trp Gly His Arg Leu Asp

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ggc ttc ccc cct ggg cgg cct tct cca gac aat ctg aac caa atc tgc 644

Gly Phe Pro Pro Gly Arg Pro Ser Pro Asp Asn Leu Asn Gln Ile Cys

170

175

180

ctt cct aac cgt cag cat gtg gta tat ggt ccc tgg aac cta cca cag 692

Leu Pro Asn Arg Gln His Val Val Tyr Gly Pro Trp Asn Leu Pro Gln

185

190

195

tcc agc tac tcc cac ctc act cgc cag ggt gag acc ctc aat ttc ctg 740

Ser Ser Tyr Ser His Leu Thr Arg Gln Gly Glu Thr Leu Asn Phe Leu

200

205

210

gag att gga tat tcc cgc tgc tgc cac tgc cgc agc cac aca aac cgc 788

Glu Ile Gly Tyr Ser Arg Cys Cys His Cys Arg Ser His Thr Asn Arg

215

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225

cta gag tgt gcc aaa ctt gtg tgg gag gaa gca atg agc cga ttc tgt 836

Leu Glu Cys Ala Lys Leu Val Trp Glu Glu Ala Met Ser Arg Phe Cys

230

235

240

245

gag gcc gag ttc tcg gtc aag acc cga ccc cac tgg tgc tgc acg cgg 884

Glu Ala Glu Phe Ser Val Lys Thr Arg Pro His Trp Cys Cys Thr Arg

250

255

260

cag ggg gag gct cgg ttc tcc tgc ttc cag gag gaa gct ccc cag cca 932

Gln Gly Glu Ala Arg Phe Ser Cys Phe Gln Glu Glu Ala Pro Gln Pro

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275

cac tac cag ctc cgg gcc tgc ccc agc cat cag cct gat att tcc tcg 980

His Tyr Gln Leu Arg Ala Cys Pro Ser His Gln Pro Asp Ile Ser Ser

280

285

290

ggt ctt gag ctg cct ttc cct cct ggg gtg ccc aca ttg gac aat atc 1028

Gly Leu Glu Leu Pro Phe Pro Pro Gly Val Pro Thr Leu Asp Asn Ile

295

300

305

aag aac atc tgc cac ctg agg cgc ttc cgc tct gtg cca cgc aac ctg 1076

Lys Asn Ile Cys His Leu Arg Arg Phe Arg Ser Val Pro Arg Asn Leu

310

315

320

325

cca gct act gac ccc cta caa agg gag ctg ctg gca ctg atc cag ctg 1124

Pro Ala Thr Asp Pro Leu Gln Arg Glu Leu Leu Ala Leu Ile Gln Leu

330

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gag agg gag ttc cag cgc tgc tgc cgc cag ggg aac aat cac acc tgt 1172

Glu Arg Glu Phe Gln Arg Cys Cys Arg Gln Gly Asn Asn His Thr Cys

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aca tgg aag gcc tgg gag gat acc ctt gac aaa tac tgt gac cgg gag 1220

Thr Trp Lys Ala Trp Glu Asp Thr Leu Asp Lys Tyr Cys Asp Arg Glu

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365

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tat gct gtg aag acc cac cac cac ttg tgt tgc cgc cac cct ccc agc 1268

Tyr Ala Val Lys Thr His His His Leu Cys Cys Arg His Pro Pro Ser

375

380

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cct act cgg gat gag tgc ttt gcc cgt cgg gct cct tac ccc aac tat 1316

Pro Thr Arg Asp Glu Cys Phe Ala Arg Arg Ala Pro Tyr Pro Asn Tyr

390

395

400

405

gac cgg gac atc ttg acc att gac atc agt cga gtc acc ccc aac ctc 1364

Asp Arg Asp Ile Leu Thr Ile Asp Ile Ser Arg Val Thr Pro Asn Leu

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415

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atg ggc cac ctc tgt gga aac caa aga gtt ctc acc aag cat aaa cat 1412

Met Gly His Leu Cys Gly Asn Gln Arg Val Leu Thr Lys His Lys His

425

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att cct ggg ctg atc cac aac atg act gcc cgc tgc tgt gac ctg cca 1460

Ile Pro Gly Leu Ile His Asn Met Thr Ala Arg Cys Cys Asp Leu Pro

440

445

450

ttt cca gaa cag gcc tgc tgt gca gag gag gag aaa tta acc ttc atc 1508

Phe Pro Glu Gln Ala Cys Cys Ala Glu Glu Glu Lys Leu Thr Phe Ile

455

460

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aat gat ctg tgt ggt ccc cga cgt aac atc tgg cga gac cct gcc ctc 1556

Asn Asp Leu Cys Gly Pro Arg Arg Asn Ile Trp Arg Asp Pro Ala Leu

470

475

480

485

tgc tgt tac ctg agt cct ggg gat gaa cag gtc aac tgc ttc aac atc 1604

Cys Cys Tyr Leu Ser Pro Gly Asp Glu Gln Val Asn Cys Phe Asn Ile

490

495

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aat tat ctg agg aac gtg gct cta gtg tct gga gac act gag aac gcc 1652

Asn Tyr Leu Arg Asn Val Ala Leu Val Ser Gly Asp Thr Glu Asn Ala

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aag ggc cag ggg gag cag ggc tca act gga gga aca aat atc agc tcc 1700

Lys Gly Gln Gly Glu Gln Gly Ser Thr Gly Gly Thr Asn Ile Ser Ser

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525

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acc tct gag ccc aag gaa gaa tgagtcaccc cagagcccta gagggtcaga 1751

Thr Ser Glu Pro Lys Glu Glu

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<212> PRT

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20

25

30

Arg Ile Leu Leu Leu Gly Thr Ala Val Glu Ser Ala Trp Gly Asp Glu

35

40

45

Gln Ser Ala Phe Arg Cys Asn Thr Gln Gln Pro Gly Cys Glu Asn Val

50

55

60

Cys Tyr Asp Lys Ser Phe Pro Ile Ser His Val Arg Phe Trp Val Leu

65

70

75

80

Gln Ile Ile Phe Val Ser Val Pro Thr Leu Leu Tyr Leu Ala His Val

85

90

95

Phe Tyr Val Met Arg Lys Glu Glu Lys Leu Asn Lys Lys Glu Glu Glu

100

105

110

Leu Lys Val Ala Gln Thr Asp Gly Val Asn Val Asp Met His Leu Lys

115

120

125

Gln Ile Glu Ile Lys Lys Phe Lys Tyr Gly Ile Glu Glu His Gly Lys

130

135

140

Val Lys Met Arg Gly Gly Leu Leu Arg Thr Tyr Ile Ile Ser Ile Leu

145

150

155

160

Phe Lys Ser Ile Phe Glu Val Ala Phe Leu Leu Ile Gln Trp Tyr Ile

165

170

175

Tyr Gly Phe Ser Leu Ser Ala Val Tyr Thr Cys Lys Arg Asp Pro Cys

180

185

190

Pro His Gln Val Asp Cys Phe Leu Ser Arg Pro Thr Glu Lys Thr Ile

195

200

205

Phe Ile Ile Phe Met Leu Val Val Ser Leu Val Ser Leu Ala Leu Asn

210

215

220

Ile Ile Glu Leu Phe Tyr Val Phe Phe Lys Gly Val Lys Asp Arg Val

225

230

235

240

Lys Gly Lys Ser Asp Pro Tyr His Ala Thr Ser Gly Ala Leu Ser Pro
 245 250 255

Ala Lys Asp Cys Gly Ser Gln Lys Tyr Ala Tyr Phe Asn Gly Cys Ser
 260 265 270

Ser Pro Thr Ala Pro Leu Ser Pro Met Ser Pro Pro Gly Tyr Lys Leu
 275 280 285

Val Thr Gly Asp Arg Asn Asn Ser Ser Cys Arg Asn Tyr Asn Lys Gln
 290 295 300

Ala Ser Glu Gln Thr Trp Ala Asn Tyr Ser Ala Glu Gln Asn Arg Met
 305 310 315 320

Gly Gln Ala Gly Ser Thr Ile Ser Asn Ser His Ala Gln Pro Phe Asp
 325 330 335

Phe Pro Asp Asp Asn Gln Asn Ser Lys Lys Leu Ala Ala Gly His Glu
 340 345 350

Leu Gln Pro Leu Ala Ile Val Asp Gln Arg Pro Ser Ser Arg Ala Ser
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Ser Arg Ala Ser Ser Arg Pro Arg Pro Asp Asp Leu Glu Ile
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attttacttc atcctccaag gagttcaatc acttggcgtg acttcactac ttttaagcaa 180

aagagtggcg cccaggcaac atg ggt gac tgg agc gcc tta ggc aaa ctc ctt 233

Met Gly Asp Trp Ser Ala Leu Gly Lys Leu Leu

1 5 10

gac aag gtt caa gcc tac tca act gct gga ggg aag gtg tgg ctg tca 281

Asp Lys Val Gln Ala Tyr Ser Thr Ala Gly Gly Lys Val Trp Leu Ser

15 20 25

gta ctt ttc att ttc cga atc ctg ctg ctg ggg aca gcg gtt gag tca 329

Val Leu Phe Ile Phe Arg Ile Leu Leu Leu Gly Thr Ala Val Glu Ser

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gcc tgg gga gat gag cag tct gcc ttt cgt tgt aac act cag caa cct 377

Ala Trp Gly Asp Glu Gln Ser Ala Phe Arg Cys Asn Thr Gln Gln Pro

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ggt tgt gaa aat gtc tgc tat gac aag tct ttc cca atc tct cat gtg 425

Gly Cys Glu Asn Val Cys Tyr Asp Lys Ser Phe Pro Ile Ser His Val

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70

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cgc ttc tgg gtc ctg cag atc ata ttt gtg tct gta ccc aca ctc ttg 473

Arg Phe Trp Val Leu Gln Ile Ile Phe Val Ser Val Pro Thr Leu Leu

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tac ctg gct cat gtg ttc tat gtg atg cga aag gaa gag aaa ctg aac 521

Tyr Leu Ala His Val Phe Tyr Val Met Arg Lys Glu Glu Lys Leu Asn

95

100

105

aag aaa gag gaa gaa ctc aag gtt gcc caa act gat ggt gtc aat gtg 569

Lys Lys Glu Glu Glu Leu Lys Val Ala Gln Thr Asp Gly Val Asn Val

110

115

120

gac atg cac ttg aag cag att gag ata aag aag ttc aag tac ggt att 617

Asp Met His Leu Lys Gln Ile Glu Ile Lys Lys Phe Lys Tyr Gly Ile

125

130

135

gaa gag cat ggt aag gtg aaa atg cga ggg ggg ttg ctg cga acc tac 665

Glu Glu His Gly Lys Val Lys Met Arg Gly Gly Leu Leu Arg Thr Tyr

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atc atc agt atc ctc ttc aag tct atc ttt gag gtg gcc ttc ttg ctg 713

Ile Ile Ser Ile Leu Phe Lys Ser Ile Phe Glu Val Ala Phe Leu Leu

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atc cag tgg tac atc tat gga ttc agc ttg agt gct gtt tac act tgc 761

Ile Gln Trp Tyr Ile Tyr Gly Phe Ser Leu Ser Ala Val Tyr Thr Cys

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aaa aga gat ccc tgc cca cat cag gtg gac tgt ttc ctc tct cgc ccc 809

Lys Arg Asp Pro Cys Pro His Gln Val Asp Cys Phe Leu Ser Arg Pro

190

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acg gag aaa acc atc ttc atc atc ttc atg ctg gtg gtg tcc ttg gtg 857

Thr Glu Lys Thr Ile Phe Ile Ile Phe Met Leu Val Val Ser Leu Val

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tcc ctg gcc ttg aat atc att gaa ctc ttc tat gtt ttc ttc aag ggc 905

Ser Leu Ala Leu Asn Ile Ile Glu Leu Phe Tyr Val Phe Phe Lys Gly

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225

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gtt aag gat cgg gtt aag gga aag agc gac cct tac cat gcg acc agt 953

Val Lys Asp Arg Val Lys Gly Lys Ser Asp Pro Tyr His Ala Thr Ser

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ggt gcg ctg agc cct gcc aaa gac tgt ggg tct caa aaa tat gct tat 1001

Gly Ala Leu Ser Pro Ala Lys Asp Cys Gly Ser Gln Lys Tyr Ala Tyr

255

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ttc aat ggc tgc tcc tca cca acc gct ccc ctc tgc cct atg tct cct 1049

Phe Asn Gly Cys Ser Ser Pro Thr Ala Pro Leu Ser Pro Met Ser Pro

270

275

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cct ggg tac aag ctg gtt act ggc gac aga aac aat tct tct tgc cgc 1097

Pro Gly Tyr Lys Leu Val Thr Gly Asp Arg Asn Asn Ser Ser Cys Arg

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aat tac aac aag caa gca agt gag caa acc tgg gct aat tac agt gca 1145

Asn Tyr Asn Lys Gln Ala Ser Glu Gln Thr Trp Ala Asn Tyr Ser Ala

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gaa caa aat cga atg ggg cag gcg gga agc acc atc tct aac tcc cat 1193

Glu Gln Asn Arg Met Gly Gln Ala Gly Ser Thr Ile Ser Asn Ser His

320

325

330

gca cag cct ttt gat ttc ccc gat gat aac cag aat tct aaa aaa cta 1241

Ala Gln Pro Phe Asp Phe Pro Asp Asp Asn Gln Asn Ser Lys Lys Leu

335

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gct gct gga cat gaa tta cag cca cta gcc att gtg gac cag cga cct 1289

Ala Ala Gly His Glu Leu Gln Pro Leu Ala Ile Val Asp Gln Arg Pro

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tca agc aga gcc agc agt cgt gcc agc agc aga cct cgg cct gat gac 1337

Ser Ser Arg Ala Ser Ser Arg Ala Ser Ser Arg Pro Arg Pro Asp Asp

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370

375

ctg gag atc tagatacagg ctigaaagca tcaagattcc actcaattgt 1386

Leu Glu Ile

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ggagaagaaa aaaggtgctg tagaaagtgc accaggtggt aattttgacg cggtggaggt 1446

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cagtttctcc aaatgccttt tttaaaactc atcacagaag attggtgaaa atgctgagta 2886

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tttagtat 3074

Abstract. We study the asymptotic behavior of the eigenvalues of the Dirac operator associated to a metric tensor field depending on a parameter λ . The limit problem is solved by means of the spectral theorem for self-adjoint operators. As an application we obtain the asymptotic expansion of the eigenvalues of the Dirac operator associated to a metric tensor field depending on a parameter λ .

[illegible]

1

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Tyr Ser Thr Ala Gly Gly Lys Val Trp Leu Ser Val Leu Phe Ile Phe

25

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Arg Ile Leu Leu Leu Gly Thr Ala Val Glu Ser Ala Trp Gly Asp Glu

40

45

Gln Ser Ala Phe Arg Cys Asn Thr Gln Gln Pro Gly Cys Glu Asn Val

55

60

Cys Tyr Asp Lys Ser Phe Pro Ile Ser His Val Arg Phe Trp Val Leu

70

75

80

Gln Ile Ile Phe Val Ser Val Pro Thr Leu Leu Tyr Leu Ala His Val

90

95

Phe Tyr Val Met Arg Lys Glu Glu Lys Leu Asn Lys Lys Glu Glu Glu

105

110

Leu Lys Val Ala Gln Thr Asp Gly Val Asn Val Asp Met His Leu Lys

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Gln Ile Glu Ile Lys Lys Phe Lys Tyr Gly Ile Glu Glu His Gly Lys

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Val Lys Met Arg Gly Gly Leu Leu Arg Thr Tyr Ile Ile Ser Ile Leu

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Phe Lys Ser Ile Phe Glu Val Ala Phe Leu Leu Ile Gln Trp Tyr Ile

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Tyr Gly Phe Ser Leu Ser Ala Val Tyr Thr Cys Lys Arg Asp Pro Cys

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185

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Pro His Gln Val Asp Cys Phe Leu Ser Arg Pro Thr Glu Lys Thr Ile

195

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205

Phe Ile Ile Phe Met Leu Val Val Ser Leu Val Ser Leu Ala Leu Asn

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215

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Ile Ile Glu Leu Phe Tyr Val Phe Phe Lys Gly Val Lys Asp Arg Val

225

230

235

240

Lys Gly Lys Ser Asp Pro Tyr His Ala Thr Ser Gly Ala Leu Ser Pro

245

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Ala Lys Asp Cys Gly Ser Gln Lys Tyr Ala Tyr Phe Asn Gly Cys Ser

260

265

270

Ser Pro Thr Ala Pro Leu Ser Pro Met Ser Pro Pro Gly Tyr Lys Leu

275 280 285

Val Thr Gly Asp Arg Asn Asn Ser Ser Cys Arg Asn Tyr Asn Lys Gln

290 295 300

Ala Ser Glu Gln Asn Trp Ala Asn Tyr Ser Ala Glu Gln Asn Arg Met

305 310 315 320

Gly Gln Ala Gly Ser Thr Ile Ser Asn Ser His Ala Gln Pro Phe Asp

325 330 335

Phe Pro Asp Asp Asn Gln Asn Ser Lys Lys Leu Ala Ala Gly His Glu

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Leu Gln Pro Leu Ala Ile Val Asp Gln Arg Pro Ser Ser Arg Ala Ser

355 360 365

Ser Arg Ala Ser Ser Arg Pro Arg Pro Asp Asp Leu Glu Ile

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<211> 3074

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (201).. (1346)

<400> 116

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attttacttc atcctccaag gagttcaatc acttggcgtg acttcactac ttttaagcaa 180

aagagtgggtg cccaggcaac atg ggt gac tgg agc gcc tta ggc aaa ctc ctt 233

Met Gly Asp Trp Ser Ala Leu Gly Lys Leu Leu

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gac aag gtt caa gcc tac tca act gct gga ggg aag gtg tgg ctg tca 281

Asp Lys Val Gln Ala Tyr Ser Thr Ala Gly Gly Lys Val Trp Leu Ser

15 20 25

gta ctt ttc att ttc cga atc ctg ctg ctg ggg aca gcg gtt gag tca 329

Val Leu Phe Ile Phe Arg Ile Leu Leu Leu Gly Thr Ala Val Glu Ser

30 35 40

gcc tgg gga gat gag cag tct gcc ttt cgt tgt aac act cag caa cct 377

Ala Trp Gly Asp Glu Gln Ser Ala Phe Arg Cys Asn Thr Gln Gln Pro

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ggt tgt gaa aat gtc tgc tat gac aag tct ttc cca atc tct cat gtg 425

Gly Cys Glu Asn Val Cys Tyr Asp Lys Ser Phe Pro Ile Ser His Val

60 65 70 75

cgc ttc tgg gtc ctg cag atc ata ttt gtg tct gta ccc aca ctc ttg 473

Arg Phe Trp Val Leu Gln Ile Ile Phe Val Ser Val Pro Thr Leu Leu

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tac ctg gct cat gtg ttc tat gtg atg cga aag gaa gag aaa ctg aac 521

Tyr Leu Ala His Val Phe Tyr Val Met Arg Lys Glu Glu Lys Leu Asn

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aag aaa gag gaa gaa ctc aag gtt gcc caa act gat ggt gtc aat gtg 569

Lys Lys Glu Glu Glu Leu Lys Val Ala Gln Thr Asp Gly Val Asn Val

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gac atg cac ttg aag cag att gag ata aag aag ttc aag tac ggt att 617

Asp Met His Leu Lys Gln Ile Glu Ile Lys Lys Phe Lys Tyr Gly Ile

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gaa gag cat ggt aag gtg aaa atg cga ggg ggg ttg ctg cga acc tac 665

Glu Glu His Gly Lys Val Lys Met Arg Gly Gly Leu Leu Arg Thr Tyr

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atc atc agt atc ctc ttc aag tct atc ttt gag gtg gcc ttc ttg ctg 713

Ile Ile Ser Ile Leu Phe Lys Ser Ile Phe Glu Val Ala Phe Leu Leu

160

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atc cag tgg tac atc tat gga ttc agc ttg agt gct gtt tac act tgc 761

Ile Gln Trp Tyr Ile Tyr Gly Phe Ser Leu Ser Ala Val Tyr Thr Cys

175

180

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aaa aga gat ccc tgc cca cat cag gtg gac tgt ttc ctc tct cgc ccc 809

Lys Arg Asp Pro Cys Pro His Gln Val Asp Cys Phe Leu Ser Arg Pro

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acg gag aaa acc atc ttc atc atc ttc atg ctg gtg gtg tcc ttg gtg 857

Thr Glu Lys Thr Ile Phe Ile Ile Phe Met Leu Val Val Ser Leu Val

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Ser Leu Ala Leu Asn Ile Ile Glu Leu Phe Tyr Val Phe Phe Lys Gly

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225

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gtt aag gat cgg gtt aag gga aag agc gac cct tac cat gcg acc agt 953

Val Lys Asp Arg Val Lys Gly Lys Ser Asp Pro Tyr His Ala Thr Ser

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ggt gcg ctg agc cct gcc aaa gac tgt ggg tct caa aaa tat gct tat 1001

Gly Ala Leu Ser Pro Ala Lys Asp Cys Gly Ser Gln Lys Tyr Ala Tyr

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cct ggg tac aag ctg gtt act ggc gac aga aac aat tct tct tgc cgc 1097

Pro Gly Tyr Lys Leu Val Thr Gly Asp Arg Asn Asn Ser Ser Cys Arg

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aat tac aac aag caa gca agt gag caa aac tgg gct aat tac agt gca 1145

Asn Tyr Asn Lys Gln Ala Ser Glu Gln Asn Trp Ala Asn Tyr Ser Ala

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310

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gaa caa aat cga atg ggg cag gcg gga agc acc atc tct aac tcc cat 1193

Glu Gln Asn Arg Met Gly Gln Ala Gly Ser Thr Ile Ser Asn Ser His

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gca cag cct ttt gat ttc ccc gat gat aac cag aat tct aaa aaa cta 1241

Ala Gln Pro Phe Asp Phe Pro Asp Asp Asn Gln Asn Ser Lys Lys Leu

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gct gct gga cat gaa tta cag cca cta gcc att gtg gac cag cga cct 1289

Ala Ala Gly His Glu Leu Gln Pro Leu Ala Ile Val Asp Gln Arg Pro

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355

360

tca agc aga gcc agc agt cgt gcc agc agc aga cct cgg cct gat gac 1337

Ser Ser Arg Ala Ser Ser Arg Ala Ser Ser Arg Pro Arg Pro Asp Asp

365

370

375

ctg gag atc tagatacagg cttgaaagca tcaagattcc actcaattgt 1386

Leu Glu Ile

380

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tcactggggg tgtatggggt agatgggtgg agaggaggag gataagagag gtgcatgttg 1566

gtatttaaag tagtggattc aaagaactta gattataaat aagagttcca ttaggtgata 1626

Met Glu Gly Ala Ala Leu Leu Arg Val Ser Val Leu Cys Ile Trp Met

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Ser Ala Leu Phe Leu Gly Val Gly Val Arg Ala Glu Glu Ala Gly Ala

20 25 30

Arg Val Gln Gln Asn Val Pro Ser Gly Thr Asp Thr Gly Asp Pro Gln

35 40 45

Ser Lys Pro Leu Gly Asp Trp Ala Ala Gly Thr Met Asp Pro Glu Ser

50 55 60

Ser Ile Phe Ile Glu Asp Ala Ile Lys Tyr Phe Lys Glu Lys Val Ser

65 70 75 80

Thr Gln Asn Leu Leu Leu Leu Leu Thr Asp Asn Glu Ala Trp Asn Gly

85 90 95

Phe Val Ala Ala Ala Glu Leu Pro Arg Asn Glu Ala Asp Glu Leu Arg

100 105 110

Lys Ala Leu Asp Asn Leu Ala Arg Gln Met Ile Met Lys Asp Lys Asn

115 120 125

Trp His Asp Lys Gly Gln Gln Tyr Arg Asn Trp Phe Leu Lys Glu Phe

130 135 140

Pro Arg Leu Lys Ser Lys Leu Glu Asp Asn Ile Arg Arg Leu Arg Ala

145 150 155 160

Leu Ala Asp Gly Val Gln Lys Val His Lys Gly Thr Thr Ile Ala Asn

165

170

175

Val Val Ser Gly Ser Leu Ser Ile Ser Ser Gly Ile Leu Thr Leu Val

180

185

190

Gly Met Gly Leu Ala Pro Phe Thr Glu Gly Gly Ser Leu Val Leu Leu

195

200

205

Glu Pro Gly Met Glu Leu Gly Ile Thr Ala Ala Leu Thr Gly Ile Thr

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215

220

Ser Ser Thr Ile Asp Tyr Gly Lys Lys Trp Trp Thr Gln Ala Gln Ala

225

230

235

240

His Asp Leu Val Ile Lys Ser Leu Asp Lys Leu Lys Glu Val Lys Glu

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255

Phe Leu Gly Glu Asn Ile Ser Asn Phe Leu Ser Leu Ala Gly Asn Thr

260

265

270

Tyr Gln Leu Thr Arg Gly Ile Gly Lys Asp Ile Arg Ala Leu Arg Arg

275

280

285

Ala Arg Ala Asn Leu Gln Ser Val Pro His Ala Ser Ala Ser Arg Pro

290

295

300

Arg Val Thr Glu Pro Ile Ser Ala Glu Ser Gly Glu Gln Val Glu Arg

414/735

all amino acids are present in the protein

305 310 315 320

Val Asn Glu Pro Ser Ile Leu Glu Met Ser Arg Gly Val Lys Leu Thr

325 330 335

Asp Val Ala Pro Val Ser Phe Phe Leu Val Leu Asp Val Val Tyr Leu

340 345 350

Val Tyr Glu Ser Lys His Leu His Glu Gly Ala Lys Ser Glu Thr Ala

355 360 365

Glu Glu Leu Lys Lys Val Ala Gln Glu Leu Glu Glu Lys Leu Asn Ile

370 375 380

Leu Asn Asn Asn Tyr Lys Ile Leu Gln Ala Asp Gln Glu Leu

385 390 395

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<212> DNA

<213> Homo sapiens

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<222> (76)..(1269)

<400> 118

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Met Glu Gly Ala Ala Leu Leu Arg Val Ser Val Leu

1 5 10

tgc atc tgg atg agt gca ctt ttc ctt ggt gtg gga gtg agg gca gag 159

Cys Ile Trp Met Ser Ala Leu Phe Leu Gly Val Gly Val Arg Ala Glu

15 20 25

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Glu Ala Gly Ala Arg Val Gln Gln Asn Val Pro Ser Gly Thr Asp Thr

30 35 40

gga gat cct caa agt aag ccc ctc ggt gac tgg gct gct ggc acc atg 255

Gly Asp Pro Gln Ser Lys Pro Leu Gly Asp Trp Ala Ala Gly Thr Met

45 50 55 60

gac cca gag agc agt atc ttt att gag gat gcc att aag tat ttc aag 303

Asp Pro Glu Ser Ser Ile Phe Ile Glu Asp Ala Ile Lys Tyr Phe Lys

65 70 75

gaa aaa gtg agc aca cag aat ctg cta ctc ctg ctg act gat aat gag 351

Glu Lys Val Ser Thr Gln Asn Leu Leu Leu Leu Leu Thr Asp Asn Glu

80 85 90

gcc tgg aac gga ttc gtg gct gct gct gaa ctg ccc agg aat gag gca 399

Ala Trp Asn Gly Phe Val Ala Ala Ala Glu Leu Pro Arg Asn Glu Ala

95 100 105

gat gag ctc cgt aaa gct ctg gac aac ctt gca aga caa atg atc atg 447

Asp Glu Leu Arg Lys Ala Leu Asp Asn Leu Ala Arg Gln Met Ile Met

110

115

120

aaa gac aaa aac tgg cac gat aaa ggc cag cag tac aga aac tgg ttt 495

Lys Asp Lys Asn Trp His Asp Lys Gly Gln Gln Tyr Arg Asn Trp Phe

125

130

135

140

ctg aaa gag ttt cct cgg ttg aaa agt aag ctt gag gat aac ata aga 543

Leu Lys Glu Phe Pro Arg Leu Lys Ser Lys Leu Glu Asp Asn Ile Arg

145

150

155

agg ctc cgt gcc ctt gca gat ggg gtt cag aag gtc cac aaa ggc acc 591

Arg Leu Arg Ala Leu Ala Asp Gly Val Gln Lys Val His Lys Gly Thr

160

165

170

acc atc gcc aat gtg gtg tct ggc tct ctc agc att tcc tct ggc atc 639

Thr Ile Ala Asn Val Val Ser Gly Ser Leu Ser Ile Ser Ser Gly Ile

175

180

185

ctg acc ctc gtc ggc atg ggt ctg gca ccc ttc aca gag gga ggc agc 687

Leu Thr Leu Val Gly Met Gly Leu Ala Pro Phe Thr Glu Gly Gly Ser

190

195

200

ctt gta ctc ttg gaa cct ggg atg gag ttg gga atc aca gca gct ttg 735

Leu Val Leu Leu Glu Pro Gly Met Glu Leu Gly Ile Thr Ala Ala Leu

205

210

215

220

acc ggg att acc agc agt acc ata gac tac gga aag aag tgg tgg aca 783

Thr Gly Ile Thr Ser Ser Thr Ile Asp Tyr Gly Lys Lys Trp Trp Thr
 225 230 235

caa gcc caa gcc cac gac ctg gtc atc aaa agc ctt gac aaa ttg aag 831
 Gln Ala Gln Ala His Asp Leu Val Ile Lys Ser Leu Asp Lys Leu Lys
 240 245 250

gag gtg aag gag ttt ttg ggt gag aac ata tcc aac ttt ctt tcc tta 879
 Glu Val Lys Glu Phe Leu Gly Glu Asn Ile Ser Asn Phe Leu Ser Leu
 255 260 265

gct ggc aat act tac caa ctc aca cga ggc att ggg aag gac atc cgt 927
 Ala Gly Asn Thr Tyr Gln Leu Thr Arg Gly Ile Gly Lys Asp Ile Arg
 270 275 280

gcc ctc aga cga gcc aga gcc aat ctt cag tca gta ccg cat gcc tca 975
 Ala Leu Arg Arg Ala Arg Ala Asn Leu Gln Ser Val Pro His Ala Ser
 285 290 295 300

gcc tca cgc ccc cgg gtc act gag cca atc tca gct gaa agc ggt gaa 1023
 Ala Ser Arg Pro Arg Val Thr Glu Pro Ile Ser Ala Glu Ser Gly Glu
 305 310 315

cag gtg gag aga gtt aat gaa ccc agc atc ctg gaa atg agc aga gga 1071
 Gln Val Glu Arg Val Asn Glu Pro Ser Ile Leu Glu Met Ser Arg Gly
 320 325 330

gtc aag ctc acg gat gtg gcc cct gta agc ttc ttt ctt gtg ctg gat 1119
 Val Lys Leu Thr Asp Val Ala Pro Val Ser Phe Phe Leu Val Leu Asp
 418/735

335

340

345

gta gtc tac ctc gtg tac gaa tca aag cac tta cat gag ggg gca aag 1167
Val Val Tyr Leu Val Tyr Glu Ser Lys His Leu His Glu Gly Ala Lys

350

355

360

tca gag aca gct gag gag ctg aag aag gtg gct cag gag ctg gag gag 1215
Ser Glu Thr Ala Glu Glu Leu Lys Lys Val Ala Gln Glu Leu Glu Glu

365

370

375

380

aag cta aac att ctc aac aat aat tat aag att ctg cag gcg gac caa 1263
Lys Leu Asn Ile Leu Asn Asn Asn Tyr Lys Ile Leu Gln Ala Asp Gln

385

390

395

gaa ctg tgaccacagg gcagggcagc caccaggaga gatatgcctg gcaggggccca 1319
Glu Leu

ggacaaaatg caaacttttt ttttttctga gacagagtct tgctctgtcg ccaagttgca 1379

gtgagccgag atatcgccac tgcactccag cctgggtgac agagegagac tccatctcaa 1439

aaaaaaaaa aaaaagaata tattgacgga agaatagaga ggaggcttga aggaaccagc 1499

aatgagaagg ccaggaaaag aaagagctga aaatggagaa agcccaagag ttagaacagt 1559

tggatacagg agaagaaaca gcggtccac tacagacca gccccaggtt caatgtcttc 1619

cgaagaatga agtctttccc tggatgatgt cccctgcct gtctttccag catccactct 1679

cccttgctct cctgggggca tatctcagtc aggcagcggc ttectgatga tggtcgttgg 1739

ggtggttgtc atgtgatggg tccccccag gttactaaag ggtgcatgtc ccctgcttga 1799

acactgaagg gcaggtggtg agccatggcc atggtcccca gctgaggagc aggtgtccct 1859

gagaacccaa acttcccaga gagtatgtga gaaccaacca atgaaaacag tcccctgct 1919

cttaccgggt aagtaaacag tcagaaaatt agcatgaaag cagtttagca ttgggaggaa 1979

gtcagatct ctagagctgt cttgtccccg cccaggattg acctgtgtaa gtcccaataa 2039

actcacctac tcatac 2054

<210> 119

<211> 398

<212> PRT

<213> Homo sapiens

<400> 119

Met Glu Gly Ala Ala Leu Leu Arg Val Ser Val Leu Cys Ile Trp Met

1 5 10 15

Ser Ala Leu Phe Leu Gly Val Arg Val Arg Ala Glu Glu Ala Gly Ala

20 25 30

Arg Val Gln Gln Asn Val Pro Ser Gly Thr Asp Thr Gly Asp Pro Gln

35 40 45

Ser Lys Pro Leu Gly Asp Trp Ala Ala Gly Thr Met Asp Pro Glu Ser
50 55 60

Ser Ile Phe Ile Glu Asp Ala Ile Lys Tyr Phe Lys Glu Lys Val Ser
65 70 75 80

Thr Gln Asn Leu Leu Leu Leu Leu Thr Asp Asn Glu Ala Trp Asn Gly
85 90 95

Phe Val Ala Ala Ala Glu Leu Pro Arg Asn Glu Ala Asp Glu Leu Arg
100 105 110

Lys Ala Leu Asp Asn Leu Ala Arg Gln Met Ile Met Lys Asp Lys Asn
115 120 125

Trp His Asp Lys Gly Gln Gln Tyr Arg Asn Trp Phe Leu Lys Glu Phe
130 135 140

Pro Arg Leu Lys Ser Lys Leu Glu Asp Asn Ile Arg Arg Leu Arg Ala
145 150 155 160

Leu Ala Asp Gly Val Gln Lys Val His Lys Gly Thr Thr Ile Ala Asn
165 170 175

Val Val Ser Gly Ser Leu Ser Ile Ser Ser Gly Ile Leu Thr Leu Val
180 185 190

Gly Met Gly Leu Ala Pro Phe Thr Glu Gly Gly Ser Leu Val Leu Leu
421/735

... ..

195

200

205

Glu Pro Gly Met Glu Leu Gly Ile Thr Ala Ala Leu Thr Gly Ile Thr

210

215

220

Ser Ser Thr Ile Asp Tyr Gly Lys Lys Trp Trp Thr Gln Ala Gln Ala

225

230

235

240

His Asp Leu Val Ile Lys Ser Leu Asp Lys Leu Lys Glu Val Lys Glu

245

250

255

Phe Leu Gly Glu Asn Ile Ser Asn Phe Leu Ser Leu Ala Gly Asn Thr

260

265

270

Tyr Gln Leu Thr Arg Gly Ile Gly Lys Asp Ile Arg Ala Leu Arg Arg

275

280

285

Ala Arg Ala Asn Leu Gln Ser Val Pro His Ala Ser Ala Ser Arg Pro

290

295

300

Arg Val Thr Glu Pro Ile Ser Ala Glu Ser Gly Glu Gln Val Glu Arg

305

310

315

320

Val Asn Glu Pro Ser Ile Leu Glu Met Ser Arg Gly Val Lys Leu Thr

325

330

335

Asp Val Ala Pro Val Ser Phe Phe Leu Val Leu Asp Val Val Tyr Leu

340

345

350

Val Tyr Glu Ser Lys His Leu His Glu Gly Ala Lys Ser Glu Thr Ala

355

360

365

Glu Glu Leu Lys Lys Val Ala Gln Glu Leu Glu Glu Lys Leu Asn Ile

370

375

380

Leu Asn Asn Asn Tyr Lys Ile Leu Gln Ala Asp Gln Glu Leu

385

390

395

<210> 120

<211> 2054

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (76)..(1269)

<400> 120

cacacagctc agaacagctg gatcttgctc agtctctgcc aggggaagat tccttggagg 60

aggccctgca gcgac atg gag gga gct gct ttg ctg aga gtc tct gtc ctc 111

Met Glu Gly Ala Ala Leu Leu Arg Val Ser Val Leu

1

5

10

tgc atc tgg atg agt gca ctt ttc ctt ggt gtg aga gtg agg gca gag 159

Cys Ile Trp Met Ser Ala Leu Phe Leu Gly Val Arg Val Arg Ala Glu

15

20

25

gaa gct gga gcg agg gtg caa caa aac gtt cca agt ggg aca gat act 207

Glu Ala Gly Ala Arg Val Gln Gln Asn Val Pro Ser Gly Thr Asp Thr

30

35

40

gga gat cct caa agt aag ccc ctc ggt gac tgg gct gct ggc acc atg 255

Gly Asp Pro Gln Ser Lys Pro Leu Gly Asp Trp Ala Ala Gly Thr Met

45

50

55

60

gac cca gag agc agt atc ttt att gag gat gcc att aag tat ttc aag 303

Asp Pro Glu Ser Ser Ile Phe Ile Glu Asp Ala Ile Lys Tyr Phe Lys

65

70

75

gaa aaa gtg agc aca cag aat ctg cta ctc ctg ctg act gat aat gag 351

Glu Lys Val Ser Thr Gln Asn Leu Leu Leu Leu Leu Thr Asp Asn Glu

80

85

90

gcc tgg aac gga ttc gtg gct gct gct gaa ctg ccc agg aat gag gca 399

Ala Trp Asn Gly Phe Val Ala Ala Ala Glu Leu Pro Arg Asn Glu Ala

95

100

105

gat gag ctc cgt aaa gct ctg gac aac ctt gca aga caa atg atc atg 447

Asp Glu Leu Arg Lys Ala Leu Asp Asn Leu Ala Arg Gln Met Ile Met

110

115

120

aaa gac aaa aac tgg cac gat aaa ggc cag cag tac aga aac tgg ttt 495

Lys Asp Lys Asn Trp His Asp Lys Gly Gln Gln Tyr Arg Asn Trp Phe

125

130

135

140

365

370

375

380

aag cta aac att ctc aac aat aat tat aag att ctg cag gcg gac caa 1263
Lys Leu Asn Ile Leu Asn Asn Asn Tyr Lys Ile Leu Gln Ala Asp Gln

385

390

395

gaa ctg tgaccacagg gcagggcagc caccaggaga gatatgcctg gcaggggcca 1319
Glu Leu

ggacaaaatg caaacttttt ttttttctga gacagagtct tgctctgtcg ccaagttgca 1379

gtgagccgag atatgccac tgcactccag cctgggtgac agagcgagac tccatctcaa 1439

aaaaaaaaa aaaaagaata tattgacgga agaatagaga ggaggettga aggaaccagc 1499

aatgagaagg ccaggaaaag aaagagctga aaatggagaa agcccaagag ttagaacagt 1559

tggatacagg agaagaaaca gcggctccac tacagacca gccccaggtt caatgtctc 1619

cgaagaatga agtctttccc tggatgatgt cccctgcctt gtctttccag catccactct 1679

cccttgctct cctgggggca tatctcagtc aggcagcggc ttcctgatga tggtcgttgg 1739

ggtggttgtc atgtgatggg tcccctccag gttactaaag ggtgcatgtc ccctgcttga 1799

acactgaagg gcaggtggtg agccatggcc atggtcccca gctgaggagc aggtgtccct 1859

gagaacccaa acttcccaga gagtatgtga gaaccaacca atgaaaacag tcccatcgct 1919

cttaccCGgt aagtaaAcag tcagaaaatt agcatgaaag cagtttagca ttgggaggaa 1979

gctcagatct ctagagctgt cttgtccccg cccaggattg acctgtgtaa gtcccaataa 2039

actcacctac tcate 2054

<210> 121

<211> 108

<212> PRT

<213> Homo sapiens

<400> 121

Met Gly Val Gln Val Glu Thr Ile Ser Pro Gly Asp Gly Arg Thr Phe

1 5 10 15

Pro Lys Arg Gly Gln Thr Cys Val Val His Tyr Thr Gly Met Leu Glu

20 25 30

Asp Gly Lys Lys Phe Asp Ser Ser Arg Asp Arg Asn Lys Pro Phe Lys

35 40 45

Phe Met Leu Gly Lys Gln Glu Val Ile Arg Gly Trp Glu Glu Gly Val

50 55 60

Ala Gln Met Ser Val Gly Gln Arg Ala Lys Leu Thr Ile Ser Pro Asp

65 70 75 80

Tyr Ala Tyr Gly Ala Thr Gly His Pro Gly Ile Ile Pro Pro His Ala

95

105

429/735

cgg gac aga aac aag ccc ttt aag ttt atg cta ggc aag cag gag gtg 256

Arg Asp Arg Asn Lys Pro Phe Lys Phe Met Leu Gly Lys Gln Glu Val

45

50

55

atc cga ggc tgg gaa gaa ggg gtt gcc cag atg agt gtg ggt cag aga 304

Ile Arg Gly Trp Glu Glu Gly Val Ala Gln Met Ser Val Gly Gln Arg

60

65

70

gcc aaa ctg act ata tct cca gat tat gcc tat ggt gcc act ggg cac 352

Ala Lys Leu Thr Ile Ser Pro Asp Tyr Ala Tyr Gly Ala Thr Gly His

75

80

85

cca ggc atc atc cca cca cat gcc act ctc gtc ttc gat gtg gag ctt 400

Pro Gly Ile Ile Pro Pro His Ala Thr Leu Val Phe Asp Val Glu Leu

90

95

100

cta aaa ctg gaa tgacaggaat ggctcctcc cttagctccc tgttcttgga 452

Leu Lys Leu Glu

105

tctgccatgg agggatctgg tgcctccaga catgtgcaca tgaatccata tggagctttt 512

cctgatgttc cactccactt tgtatagaca tctgccctga ctgaatgtgt tctgtcactc 572

agctttgctt ccgacacctc tgtttcctct tcccctttct cctegtatgt gtgtttacct 632

aaactatatg ccataaacct caagttactc attttatitt gttttcattt tgggggtgaag 692

attcagtttc agtcttttgg atataggttt ccaattaagt acatgggtcaa gtattaacag 752

cacaagtggg aggttaacat tagaatagga attgggtgtg gggggggggg ttgcaagaat 812

atattatattt aattttttgg atgaaatttt tatctattat atattaaaca ttcttgctgc 872

tgcgctgcaa agccatagca gatttgagge gctgttgagg actgaattac tctccaagtt 932

gagagatgtc ttgggttaa attaaaagcc ctacctaaaa ctgaggtggg gatggggaga 992

gcctttgcct ccaccattcc caccaccct ccccttaaac cctctgcctt tgaaagtaga 1052

tcattgtcac tgcaatgctg gacactacag gtatctgtcc ctgggccagc aggacctct 1112

gaagccttct ttgtggcctt tttttttttt tcactctgtg gtttttctaa tggactttca 1172

ggaattttgt aatctcataa ctttccaage tccaccactt cctaaatctt aagaacttta 1232

attgacagtt tcaattgaag gtgctgtttg tagacttaac acccagtgaag agcccagcca 1292

tcattgacaaa tccttgaatg ttctcttaag aaaatgatgc tggatcatgc agcttcagca 1352

tctctgttt ttgatgctt ggctccctct gctgatctca gtttcttggc ttttctccc 1412

tcagccctt ctcaccctt tgcgtctctg tgtagtgatt tggtagagaaa tcgttgctgc 1472

acccttccc cagcaccatt tatgagtctc aagttttatt attgcaataa aagtgtttta 1532

tgccggttt tctc

1546

.. .. .
.. .. .

<210> 123

<211> 679

<212> PRT

<213> Homo sapiens

<400> 123

Met Ala Thr Leu Ile Thr Ser Thr Thr Ala Ala Thr Ala Ala Ser Gly

1 5 10 15

Pro Leu Val Asp Tyr Leu Trp Met Leu Ile Leu Gly Phe Ile Ile Ala

20 25 30

Phe Val Leu Ala Phe Ser Val Gly Ala Asn Asp Val Ala Asn Ser Phe

35 40 45

Gly Thr Ala Val Gly Ser Gly Val Val Thr Leu Lys Gln Ala Cys Ile

50 55 60

Leu Ala Ser Ile Phe Glu Thr Val Gly Ser Val Leu Leu Gly Ala Lys

65 70 75 80

Val Ser Glu Thr Ile Arg Lys Gly Leu Ile Asp Val Glu Met Tyr Asn

85 90 95

Ser Thr Gln Gly Leu Leu Met Ala Gly Ser Val Ser Ala Met Phe Gly

100 105 110

Ser Ala Val Trp Gln Leu Val Ala Ser Phe Leu Lys Leu Pro Ile Ser
115 120 125

Gly Thr His Cys Ile Val Gly Ala Thr Ile Gly Phe Ser Leu Val Ala
130 135 140

Lys Gly Gln Glu Gly Val Lys Trp Ser Glu Leu Ile Lys Ile Val Met
145 150 155 160

Ser Trp Phe Val Ser Pro Leu Leu Ser Gly Ile Met Ser Gly Ile Leu
165 170 175

Phe Phe Leu Val Arg Ala Phe Ile Leu His Lys Ala Asp Pro Val Pro
180 185 190

Asn Gly Leu Arg Ala Leu Pro Val Phe Tyr Ala Cys Thr Val Gly Ile
195 200 205

Asn Leu Phe Ser Ile Met Tyr Thr Gly Ala Pro Leu Leu Gly Phe Asp
210 215 220

Lys Leu Pro Leu Trp Gly Thr Ile Leu Ile Ser Val Gly Cys Ala Val
225 230 235 240

Phe Cys Ala Leu Ile Val Trp Phe Phe Val Cys Pro Arg Met Lys Arg
245 250 255

Lys Ile Glu Arg Glu Ile Lys Cys Ser Pro Ser Glu Ser Pro Leu Met
260 265 270

Glu Lys Lys Asn Ser Leu Lys Glu Asp His Glu Glu Thr Lys Leu Ser

275

280

285

Val Gly Asp Ile Glu Asn Lys His Pro Val Ser Glu Val Gly Pro Ala

290

295

300

Thr Val Pro Leu Gln Ala Val Val Glu Glu Arg Thr Val Ser Phe Lys

305

310

315

320

Leu Gly Asp Leu Glu Glu Ala Pro Glu Arg Glu Arg Leu Pro Ser Val

325

330

335

Asp Leu Lys Glu Glu Thr Ser Ile Asp Ser Thr Val Asn Gly Ala Val

340

345

350

Gln Leu Pro Asn Gly Asn Leu Val Gln Phe Ser Gln Ala Val Ser Asn

355

360

365

Gln Ile Asn Ser Ser Gly His Tyr Gln Tyr His Thr Val His Lys Asp

370

375

380

Ser Gly Leu Tyr Lys Glu Leu Leu His Lys Leu His Leu Ala Lys Val

385

390

395

400

Gly Asp Cys Met Gly Asp Ser Gly Asp Lys Pro Leu Arg Arg Asn Asn

405

410

415

Ser Tyr Thr Ser Tyr Thr Met Ala Ile Cys Gly Met Pro Leu Asp Ser

434/735

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420

425

430

Phe Arg Ala Lys Glu Gly Glu Gln Lys Gly Glu Glu Met Glu Lys Leu

435

440

445

Thr Trp Pro Asn Ala Asp Ser Lys Lys Arg Ile Arg Met Asp Ser Tyr

450

455

460

Thr Ser Tyr Cys Asn Ala Val Ser Asp Leu His Ser Ala Ser Glu Ile

465

470

475

480

Asp Met Ser Val Lys Ala Glu Met Gly Leu Gly Asp Arg Lys Gly Ser

485

490

495

Asn Gly Ser Leu Glu Glu Trp Tyr Asp Gln Asp Lys Pro Glu Val Ser

500

505

510

Leu Leu Phe Gln Phe Leu Gln Ile Leu Thr Ala Cys Phe Gly Ser Phe

515

520

525

Ala His Gly Gly Asn Asp Val Ser Asn Ala Ile Gly Pro Leu Val Ala

530

535

540

Leu Tyr Leu Val Tyr Asp Thr Gly Asp Val Ser Ser Lys Val Ala Thr

545

550

555

560

Pro Ile Trp Leu Leu Leu Tyr Gly Gly Val Gly Ile Cys Val Gly Leu

565

570

575

Trp Val Trp Gly Arg Arg Val Ile Gln Thr Met Gly Lys Asp Leu Thr
580 585 590

Pro Ile Thr Pro Ser Ser Gly Phe Ser Ile Glu Leu Ala Ser Ala Leu
595 600 605

Thr Val Val Ile Ala Ser Asn Ile Gly Leu Pro Ile Ser Thr Thr His
610 615 620

Cys Lys Val Gly Ser Val Val Ser Val Gly Trp Leu Arg Ser Lys Lys
625 630 635 640

Ala Val Asp Trp Arg Leu Phe Arg Asn Ile Phe Met Ala Trp Phe Val
645 650 655

Thr Val Pro Ile Ser Gly Val Ile Ser Ala Ala Ile Met Ala Ile Phe
660 665 670

Arg Tyr Val Ile Leu Arg Met
675

- <210> 124
- <211> 2916
- <212> DNA
- <213> Homo sapiens

- <220>
- <221> CDS

<222> (81).. (2117)

<400> 124

tttttgatac ctcatattct gtttacacat ctgaaaggc gtcagtagt tctcttacta 60

aacaaccact actccagaga atg gca acg ctg att acc agt act aca gct gct 113

Met Ala Thr Leu Ile Thr Ser Thr Thr Ala Ala

1 5 10

acc gcc gct tct ggt cct ttg gtg gac tac cta tgg atg ctc atc ctg 161

Thr Ala Ala Ser Gly Pro Leu Val Asp Tyr Leu Trp Met Leu Ile Leu

15 20 25

ggc ttc att att gca ttt gtc ttg gca ttc tcc gtg gga gcc aat gat 209

Gly Phe Ile Ile Ala Phe Val Leu Ala Phe Ser Val Gly Ala Asn Asp

30 35 40

gta gca aat tct ttt ggt aca gct gtg ggc tca ggt gta gtg acc ctg 257

Val Ala Asn Ser Phe Gly Thr Ala Val Gly Ser Gly Val Val Thr Leu

45 50 55

aag caa gcc tgc atc cta gct agc atc ttt gaa aca gtg ggc tct gtc 305

Lys Gln Ala Cys Ile Leu Ala Ser Ile Phe Glu Thr Val Gly Ser Val

60 65 70 75

tta ctg ggg gcc aaa gtg agc gaa acc atc cgg aag ggc ttg att gac 353

Leu Leu Gly Ala Lys Val Ser Glu Thr Ile Arg Lys Gly Leu Ile Asp

80 85 90

gtg gag atg tac aac tcg act caa ggg ctg ctg atg gcc ggc tca gtc 401

Val Glu Met Tyr Asn Ser Thr Gln Gly Leu Leu Met Ala Gly Ser Val

95

100

105

agt gct atg ttt ggt tct gct gtg tgg caa ctc gtg gct tcg ttt ttg 449

Ser Ala Met Phe Gly Ser Ala Val Trp Gln Leu Val Ala Ser Phe Leu

110

115

120

aag ctc cct att tct gga acc cat tgt att gtt ggt gca act att ggt 497

Lys Leu Pro Ile Ser Gly Thr His Cys Ile Val Gly Ala Thr Ile Gly

125

130

135

ttc tcc ctc gtg gca aag ggg cag gag ggt gtc aag tgg tct gaa ctg 545

Phe Ser Leu Val Ala Lys Gly Gln Glu Gly Val Lys Trp Ser Glu Leu

140

145

150

155

ata aaa att gtg atg tct tgg ttc gtg tcc cca ctg ctt tct gga att 593

Ile Lys Ile Val Met Ser Trp Phe Val Ser Pro Leu Leu Ser Gly Ile

160

165

170

atg tct gga att tta ttc ttc ctg gtt cgt gca ttc atc ctc cat aag 641

Met Ser Gly Ile Leu Phe Phe Leu Val Arg Ala Phe Ile Leu His Lys

175

180

185

gca gat cca gtt cct aat ggt ttg cga gct ttg cca gtt ttc tat gcc 689

Ala Asp Pro Val Pro Asn Gly Leu Arg Ala Leu Pro Val Phe Tyr Ala

190

195

200

tgc aca gtt gga ata aac ctc ttt tcc atc atg tat act gga gca ccg 737

Cys Thr Val Gly Ile Asn Leu Phe Ser Ile Met Tyr Thr Gly Ala Pro

205

210

215

ttg ctg ggc ttt gac aaa ctt cct ctg tgg ggt acc atc ctc atc tcg 785

Leu Leu Gly Phe Asp Lys Leu Pro Leu Trp Gly Thr Ile Leu Ile Ser

220

225

230

235

gtg gga tgt gca gtt ttc tgt gcc ctt atc gtc tgg ttc ttt gta tgt 833

Val Gly Cys Ala Val Phe Cys Ala Leu Ile Val Trp Phe Phe Val Cys

240

245

250

ccc agg atg aag aga aaa att gaa cga gaa ata aag tgt agt cct tct 881

Pro Arg Met Lys Arg Lys Ile Glu Arg Glu Ile Lys Cys Ser Pro Ser

255

260

265

gaa agc ccc tta atg gaa aaa aag aat agc ttg aaa gaa gac cat gaa 929

Glu Ser Pro Leu Met Glu Lys Lys Asn Ser Leu Lys Glu Asp His Glu

270

275

280

gaa aca aag ttg tct gtt ggt gat att gaa aac aag cat cct gtt tct 977

Glu Thr Lys Leu Ser Val Gly Asp Ile Glu Asn Lys His Pro Val Ser

285

290

295

gag gta ggg cct gcc act gtg ccc ctc cag gct gtg gtg gag gag aga 1025

Glu Val Gly Pro Ala Thr Val Pro Leu Gln Ala Val Val Glu Glu Arg

300

305

310

315

aca gtc tca ttc aaa ctt gga gat ttg gag gaa gct cca gag aga gag 1073

Thr Val Ser Phe Lys Leu Gly Asp Leu Glu Glu Ala Pro Glu Arg Glu

320

325

330

agg ctt ccc agc gtg gac ttg aaa gag gaa acc agc ata gat agc acc 1121

Arg Leu Pro Ser Val Asp Leu Lys Glu Glu Thr Ser Ile Asp Ser Thr

335

340

345

gtg aat ggt gca gtg cag ttg cct aat ggg aac ctt gtc cag ttc agt 1169

Val Asn Gly Ala Val Gln Leu Pro Asn Gly Asn Leu Val Gln Phe Ser

350

355

360

caa gcc gtc agc aac caa ata aac tcc agt ggc cac tac cag tat cac 1217

Gln Ala Val Ser Asn Gln Ile Asn Ser Ser Gly His Tyr Gln Tyr His

365

370

375

acc gtg cat aag gat tcc ggc ctg tac aaa gag cta ctc cat aaa tta 1265

Thr Val His Lys Asp Ser Gly Leu Tyr Lys Glu Leu Leu His Lys Leu

380

385

390

395

cat ctt gcc aag gtg gga gat tgc atg gga gac tcc ggt gac aaa ccc 1313

His Leu Ala Lys Val Gly Asp Cys Met Gly Asp Ser Gly Asp Lys Pro

400

405

410

tta agg cgc aat aat agc tat act tcc tat acc atg gca ata tgt ggc 1361

Leu Arg Arg Asn Asn Ser Tyr Thr Ser Tyr Thr Met Ala Ile Cys Gly

415

420

425

atg cct ctg gat tca ttc cgt gcc aaa gaa ggt gaa cag aag ggc gaa 1409

Met Pro Leu Asp Ser Phe Arg Ala Lys Glu Gly Glu Gln Lys Gly Glu

430

435

440

440/735

gaa atg gag aag ctg aca tgg cct aat gca gac tcc aag aag cga att 1457

Glu Met Glu Lys Leu Thr Trp Pro Asn Ala Asp Ser Lys Lys Arg Ile

445

450

455

cga atg gac agt tac acc agt tac tgc aat gct gtg tct gac ctt cac 1505

Arg Met Asp Ser Tyr Thr Ser Tyr Cys Asn Ala Val Ser Asp Leu His

460

465

470

475

tca gca tct gag ata gac atg agt gtc aag gca gag atg ggt cta ggt 1553

Ser Ala Ser Glu Ile Asp Met Ser Val Lys Ala Glu Met Gly Leu Gly

480

485

490

gac aga aaa gga agt aat ggc tct cta gaa gaa tgg tat gac cag gat 1601

Asp Arg Lys Gly Ser Asn Gly Ser Leu Glu Glu Trp Tyr Asp Gln Asp

495

500

505

aag cct gaa gtc tct ctc ctc ttc cag ttc ctg cag atc ctt aca gcc 1649

Lys Pro Glu Val Ser Leu Leu Phe Gln Phe Leu Gln Ile Leu Thr Ala

510

515

520

tgc ttt ggg tca ttc gcc cat ggt ggc aat gac gta agc aat gcc att 1697

Cys Phe Gly Ser Phe Ala His Gly Gly Asn Asp Val Ser Asn Ala Ile

525

530

535

ggg cct ctg gtt gct tta tat ttg gtt tat gac aca gga gat gtt tct 1745

Gly Pro Leu Val Ala Leu Tyr Leu Val Tyr Asp Thr Gly Asp Val Ser

540

545

550

555

tca aaa gtg gca aca cca ata tgg ctt cta ctc tat ggt ggt gtt ggt 1793

Ser Lys Val Ala Thr Pro Ile Trp Leu Leu Leu Tyr Gly Gly Val Gly

560

565

570

atc tgt gtt ggt ctg tgg gtt tgg gga aga aga gtt atc cag acc atg 1841

Ile Cys Val Gly Leu Trp Val Trp Gly Arg Arg Val Ile Gln Thr Met

575

580

585

ggg aag gat ctg aca ccg atc aca ccc tct agt ggc ttc agt att gaa 1889

Gly Lys Asp Leu Thr Pro Ile Thr Pro Ser Ser Gly Phe Ser Ile Glu

590

595

600

ctg gca tct gcc ctc act gtg gtg att gca tca aat att ggc ctt ccc 1937

Leu Ala Ser Ala Leu Thr Val Val Ile Ala Ser Asn Ile Gly Leu Pro

605

610

615

atc agt aca aca cat tgt aaa gtg ggc tct gtt gtg tct gtt ggc tgg 1985

Ile Ser Thr Thr His Cys Lys Val Gly Ser Val Val Ser Val Gly Trp

620

625

630

635

ctc cgg tcc aag aag gct gtt gac tgg cgt ctc ttt cgt aac att ttt 2033

Leu Arg Ser Lys Lys Ala Val Asp Trp Arg Leu Phe Arg Asn Ile Phe

640

645

650

atg gcc tgg ttt gtc aca gtc cct att tct gga gtt atc agt gct gcc 2081

Met Ala Trp Phe Val Thr Val Pro Ile Ser Gly Val Ile Ser Ala Ala

655

660

665

atc atg gca atc ttc aga tat gtc atc ctc aga atg tgaagctgtt 2127

Ile Met Ala Ile Phe Arg Tyr Val Ile Leu Arg Met

670

675

tgagattaaa atttgtgtca atgtttggga ccatcttagg tattcctgct cccctgaaga 2187

atgattacag tgttaacaga agactgacaa gagtcttttt atttgggagc cagaggaggg 2247

aagtgttact tgtgtataa ctgcttttgt gctaaatatg aattgtctca aaattagctg 2307

tgtaaaatag cccgggttcc actggctcct gctgaggtec cctttccttc tgggctgtga 2367

attcctgtac atatttctct actttttgta tcaggcttca attccattat gttttaatgt 2427

tgtctctgaa gatgacttgt gatttttttt tctttttttt aaaccatgaa gagccgtttg 2487

acagagcatg ctctgcgttg ttggtttcac cagcttctgc cctcacatgc acagggattt 2547

aacaacaaaa atataactac aacttcctt gtagtctctt atataagtag agtccttggt 2607

actctgccct cctgtcagta gtggcaggat ctattggcat attcgggagc ttcttagagg 2667

gatgaggttc tttgaacaca gtgaaaattt aaattagtaa cttttttgca agcagtttat 2727

tgactgttat tgctaagaag aagtaagaaa gaaaaagcct gttggcaatc ttggttattt 2787

ctttaagatt tctggcagtg tgggatggat gaatgaagtg gaatgtgaac tttgggcaag 2847

ttaaattggga cagccttcca tgttcatttg tctacctctt aactgaataa aaaagcctac 2907

agtttttag

2916

<210> 125

<211> 288

<212> PRT

<213> Homo sapiens

<400> 125

Met Glu Arg Pro Gln Pro Asp Ser Met Pro Gln Asp Leu Ser Glu Ala

1

5

10

15

Leu Lys Glu Ala Thr Lys Glu Val His Thr Gln Ala Glu Asn Ala Glu

20

25

30

Phe Met Arg Asn Phe Gln Lys Gly Gln Val Thr Arg Asp Gly Phe Lys

35

40

45

Leu Val Met Ala Ser Leu Tyr His Ile Tyr Val Ala Leu Glu Glu Glu

50

55

60

Ile Glu Arg Asn Lys Glu Ser Pro Val Phe Ala Pro Val Tyr Phe Pro

65

70

75

80

Glu Glu Leu His Arg Lys Ala Ala Leu Glu Gln Asp Leu Ala Phe Trp

85

90

95

Tyr Gly Pro Arg Trp Gln Glu Val Ile Pro Tyr Thr Pro Ala Met Gln

100

105

110

444/735

Arg Tyr Val Lys Arg Leu His Glu Val Gly Arg Thr Glu Pro Glu Leu

115

120

125

Leu Val Ala His Ala Tyr Thr Arg Tyr Leu Gly Asp Leu Ser Gly Gly

130

135

140

Gln Val Leu Lys Lys Ile Ala Gln Lys Ala Leu Asp Leu Pro Ser Ser

145

150

155

160

Gly Glu Gly Leu Ala Phe Phe Thr Phe Pro Asn Ile Ala Ser Ala Thr

165

170

175

Lys Phe Lys Gln Leu Tyr Arg Ser Arg Met Asn Ser Leu Glu Met Thr

180

185

190

Pro Ala Val Arg Gln Arg Val Ile Glu Glu Ala Lys Thr Ala Phe Leu

195

200

205

Leu Asn Ile Gln Leu Phe Glu Glu Leu Gln Glu Leu Leu Thr His Asp

210

215

220

Thr Lys Asp Gln Ser Pro Ser Arg Ala Pro Gly Leu Arg Gln Arg Ala

225

230

235

240

Ser Asn Lys Val Gln Asp Ser Ala Pro Val Glu Thr Pro Arg Gly Lys

245

250

255

Pro Pro Leu Asn Thr Arg Ser Gln Ala Pro Leu Leu Arg Trp Val Leu

445/735

260

265

270

Thr Leu Ser Phe Leu Val Ala Thr Val Ala Val Gly Leu Tyr Ala Met

275

280

285

<210> 126

<211> 1550

<212> DNA

<213> Homo sapiens

 $\langle 220 \rangle$

<221> CDS

<222> (81).. (944)

<400> 126

tcaacgcctg cctccccctcg agcgctcctca ggcgcagccgc cgccccgcgga gccagcacga 60

acgagcccag caccggccgg atg gag cgt ccg caa ccc gac agc atg ccc cag 113

Met Glu Arg Pro Gln Pro Asp Ser Met Pro Gln

1

5

10

gat ttg tca gag gcc ctg aag gag gcc acc aag gag gtg cac acc cag 161

Asp Leu Ser Glu Ala Leu Lys Glu Ala Thr Lys Glu Val His Thr Gln

15

20

25

gca gag aat gct gag ttc atg agg aac ttt cag aag ggc cag gtg acc 209

Ala Glu Asn Ala Glu Phe Met Arg Asn Phe Gln Lys Gly Gln Val Thr

30

35

40

446/735

cga gac ggc ttc aag ctg gtg atg gcc tcc ctg tac cac atc tat gtg 257

Arg Asp Gly Phe Lys Leu Val Met Ala Ser Leu Tyr His Ile Tyr Val

45 50 55

gcc ctg gag gag gag att gag cgc aac aag gag agc cca gtc ttc gcc 305

Ala Leu Glu Glu Glu Ile Glu Arg Asn Lys Glu Ser Pro Val Phe Ala

60 65 70 75

cct gtc tac ttc cca gaa gag ctg cac cgc aag gct gcc ctg gag cag 353

Pro Val Tyr Phe Pro Glu Glu Leu His Arg Lys Ala Ala Leu Glu Gln

80 85 90

gac ctg gcc ttc tgg tac ggg ccc cgc tgg cag gag gtc atc ccc tac 401

Asp Leu Ala Phe Trp Tyr Gly Pro Arg Trp Gln Glu Val Ile Pro Tyr

95 100 105

aca cca gcc atg cag cgc tat gtg aag cgg ctc cac gag gtg ggg cgc 449

Thr Pro Ala Met Gln Arg Tyr Val Lys Arg Leu His Glu Val Gly Arg

110 115 120

aca gag ccc gag ctg ctg gtg gcc cac gcc tac acc cgc tac ctg ggt 497

Thr Glu Pro Glu Leu Leu Val Ala His Ala Tyr Thr Arg Tyr Leu Gly

125 130 135

gac ctg tct ggg ggc cag gtg ctc aaa aag att gcc cag aaa gcc ctg 545

Asp Leu Ser Gly Gly Gln Val Leu Lys Lys Ile Ala Gln Lys Ala Leu

140 145 150 155

gac ctg ccc agc tct ggc gag ggc ctg gcc ttc ttc acc ttc ccc aac 593

Asp Leu Pro Ser Ser Gly Glu Gly Leu Ala Phe Phe Thr Phe Pro Asn

160

165

170

att gcc agt gcc acc aag ttc aag cag ctc tac cgc tcc cgc atg aac 641

Ile Ala Ser Ala Thr Lys Phe Lys Gln Leu Tyr Arg Ser Arg Met Asn

175

180

185

tcc ctg gag atg act ccc gca gtc agg cag agg gtg ata gaa gag gcc 689

Ser Leu Glu Met Thr Pro Ala Val Arg Gln Arg Val Ile Glu Glu Ala

190

195

200

aag act gcg ttc ctg ctc aac atc cag ctc ttt gag gag ttg cag gag 737

Lys Thr Ala Phe Leu Leu Asn Ile Gln Leu Phe Glu Glu Leu Gln Glu

205

210

215

ctg ctg acc cat gac acc aag gac cag agc ccc tca cgg gca cca ggg 785

Leu Leu Thr His Asp Thr Lys Asp Gln Ser Pro Ser Arg Ala Pro Gly

220

225

230

235

ctt cgc cag cgg gcc agc aac aaa gtg caa gat tct gcc ccc gtg gag 833

Leu Arg Gln Arg Ala Ser Asn Lys Val Gln Asp Ser Ala Pro Val Glu

240

245

250

act ccc aga ggg aag ccc cca ctc aac acc cgc tcc cag gct ccg ctt 881

Thr Pro Arg Gly Lys Pro Pro Leu Asn Thr Arg Ser Gln Ala Pro Leu

255

260

265

ctc cga tgg gtc ctt aca ctc agc ttt ctg gtg gcg aca gtt get gta 929

448/735

Leu Arg Trp Val Leu Thr Leu Ser Phe Leu Val Ala Thr Val Ala Val

270

275

280

ggg ctt tat gcc atg tgaatgcagg catgctggct cccagggcca tgaactttgt 984

Gly Leu Tyr Ala Met

285

ccggtggaag gccttctttc tagagaggga attctcttgg ctggettctt taccgtgggc 1044

actgaaggct ttcagggcct ccagccctct cactgtgtcc ctctctctgg aaaggaggaa 1104

ggagcctatg gcattctccc caacgaaaag cacatccagg caatggccta aacttcagag 1164

ggggcgaagg ggtcagccct gcccttcagc atcctcagtt cctgcagcag agcctggaag 1224

acacccta atgtggcagctg tctcaaacct ccaaaagccc tgagtttcaa gtatccttgt 1284

tgacacggcc atgaccactt tccccgtggg ccatggcaat ttttacacaa acctgaaaag 1344

atgttggtgc ttgtgttttt gtcttatatt tggtggagcc actctgttcc tggctcagcc 1404

tcaaatgcag tattttttgtt gtgttctgtt gtttttatag cagggttggg gtggtttttg 1464

agccatgcgt ggggtggggag ggaggtgttt aacggcactg tggccttggt ctaacttttg 1524

tgtgaaataa taaacaacat tgtctg 1550

<211> 135

<212> PRT

<213> Homo sapiens

<400> 127

Met Ala Cys Gly Leu Val Ala Ser Asn Leu Asn Leu Lys Pro Gly Glu

1 5 10 15

Cys Leu Arg Val Arg Gly Glu Val Ala Pro Asp Ala Lys Ser Phe Val

20 25 30

Leu Asn Leu Gly Lys Asp Ser Asn Asn Leu Cys Leu His Phe Asn Pro

35 40 45

Arg Phe Asn Ala His Gly Asp Ala Asn Thr Ile Val Cys Asn Ser Lys

50 55 60

Asp Gly Gly Ala Trp Gly Thr Glu Gln Arg Glu Ala Val Phe Pro Phe

65 70 75 80

Gln Pro Gly Ser Val Ala Glu Val Cys Ile Thr Phe Asp Gln Ala Asn

85 90 95

Leu Thr Val Lys Leu Pro Asp Gly Tyr Glu Phe Lys Phe Pro Asn Arg

100 105 110

Leu Asn Leu Glu Ala Ile Asn Tyr Met Ala Ala Asp Gly Asp Phe Lys

115 120 125

Ile Lys Cys Val Ala Phe Asp

130

135

<210> 128

<211> 507

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (50)..(454)

<400> 128

cttctgacag ctggtgcgcc tgcccgggaa catcctcctg gactcaatc atg gct tgt 58

Met Ala Cys

1

ggt ctg gtc gcc agc aac ctg aat ctc aaa cct gga gag tgc ctt cga 106

Gly Leu Val Ala Ser Asn Leu Asn Leu Lys Pro Gly Glu Cys Leu Arg

5

10

15

gtg cga ggc gag gtg gct cct gac gct aag agc ttc gtg ctg aac ctg 154

Val Arg Gly Glu Val Ala Pro Asp Ala Lys Ser Phe Val Leu Asn Leu

20

25

30

35

ggc aaa gac agc aac aac ctg tgc ctg cac ttc aac cct cgc ttc aac 202

Gly Lys Asp Ser Asn Asn Leu Cys Leu His Phe Asn Pro Arg Phe Asn

40

45

50

451/735

gcc cac ggc gac gcc aac acc atc gtg tgc aac agc aag gac ggc ggg 250

Ala His Gly Asp Ala Asn Thr Ile Val Cys Asn Ser Lys Asp Gly Gly

55

60

65

gcc tgg ggg acc gag cag cgg gag gct gtc ttt ccc ttc cag cct gga 298

Ala Trp Gly Thr Glu Gln Arg Glu Ala Val Phe Pro Phe Gln Pro Gly

70

75

80

agt gtt gca gag gtg tgc atc acc ttc gac cag gcc aac ctg acc gtc 346

Ser Val Ala Glu Val Cys Ile Thr Phe Asp Gln Ala Asn Leu Thr Val

85

90

95

aag ctg cca gat gga tac gaa ttc aag ttc ccc aac cgc ctc aac ctg 394

Lys Leu Pro Asp Gly Tyr Glu Phe Lys Phe Pro Asn Arg Leu Asn Leu

100

105

110

115

gag gcc atc aac tac atg gca gct gac ggt gac ttc aag atc aaa tgt 442

Glu Ala Ile Asn Tyr Met Ala Ala Asp Gly Asp Phe Lys Ile Lys Cys

120

125

130

gtg gcc ttt gac tgaaatcagc cagcccatgg cccccaataa aggcagctgc 494

Val Ala Phe Asp

135

ctctgctccc ctg

507

<210> 129

452/735

<211> 662

<212> PRT

<213> Homo sapiens

<400> 129

Met Asn Lys Glu Ile Pro Asn Gly Asn Thr Ser Glu Leu Ile Phe Asn

1 5 10 15

Ala Val His Val Lys Asp Ala Gly Phe Tyr Val Cys Arg Val Asn Asn

20 25 30

Asn Phe Thr Phe Glu Phe Ser Gln Trp Ser Gln Leu Asp Val Cys Asp

35 40 45

Ile Pro Glu Ser Phe Gln Arg Ser Val Asp Gly Val Ser Glu Ser Lys

50 55 60

Leu Gln Ile Cys Val Glu Pro Thr Ser Gln Lys Leu Met Pro Gly Ser

65 70 75 80

Thr Leu Val Leu Gln Cys Val Ala Val Gly Ser Pro Ile Pro His Tyr

85 90 95

Gln Trp Phe Lys Asn Glu Leu Pro Leu Thr His Glu Thr Lys Lys Leu

100 105 110

Tyr Met Val Pro Tyr Val Asp Leu Glu His Gln Gly Thr Tyr Trp Cys

115 120 125

His Val Tyr Asn Asp Arg Asp Ser Gln Asp Ser Lys Lys Val Glu Ile

130

135

140

Ile Ile Gly Arg Thr Asp Glu Ala Val Glu Cys Thr Glu Asp Glu Leu

145

150

155

160

Asn Asn Leu Gly His Pro Asp Asn Lys Glu Gln Thr Thr Asp Gln Pro

165

170

175

Leu Ala Lys Asp Lys Val Ala Leu Leu Ile Gly Asn Met Asn Tyr Arg

180

185

190

Glu His Pro Lys Leu Lys Ala Pro Leu Val Asp Val Tyr Glu Leu Thr

195

200

205

Asn Leu Leu Arg Gln Leu Asp Phe Lys Val Val Ser Leu Leu Asp Leu

210

215

220

Thr Glu Tyr Glu Met Arg Asn Ala Val Asp Glu Phe Leu Leu Leu Leu

225

230

235

240

Asp Lys Gly Val Tyr Gly Leu Leu Tyr Tyr Ala Gly His Gly Tyr Glu

245

250

255

Asn Phe Gly Asn Ser Phe Met Val Pro Val Asp Ala Pro Asn Pro Tyr

260

265

270

Arg Ser Glu Asn Cys Leu Cys Val Gln Asn Ile Leu Lys Leu Met Gln

275

280

285

454/735

Glu Lys Glu Thr Gly Leu Asn Val Phe Leu Leu Asp Met Cys Arg Lys

290

295

300

Arg Asn Asp Tyr Asp Asp Thr Ile Pro Ile Leu Asp Ala Leu Lys Val

305

310

315

320

Thr Ala Asn Ile Val Phe Gly Tyr Ala Thr Cys Gln Gly Ala Glu Ala

325

330

335

Phe Glu Ile Gln His Ser Gly Leu Ala Asn Gly Ile Phe Met Lys Phe

340

345

350

Leu Lys Asp Arg Leu Leu Glu Asp Lys Lys Ile Thr Val Leu Leu Asp

355

360

365

Glu Val Ala Glu Asp Met Gly Lys Cys His Leu Thr Lys Gly Lys Gln

370

375

380

Ala Leu Glu Ile Arg Ser Ser Leu Ser Glu Lys Arg Ala Leu Thr Asp

385

390

395

400

Pro Ile Gln Gly Thr Glu Tyr Ser Ala Glu Ser Leu Val Arg Asn Leu

405

410

415

Gln Trp Ala Lys Ala His Glu Leu Pro Glu Ser Met Cys Leu Lys Phe

420

425

430

Asp Cys Gly Val Gln Ile Gln Leu Gly Phe Ala Ala Glu Phe Ser Asn

455/735

.....

435

440

445

Val Met Ile Ile Tyr Thr Ser Ile Val Tyr Lys Pro Pro Glu Ile Ile

450

455

460

Met Cys Asp Ala Tyr Val Thr Asp Phe Pro Leu Asp Leu Asp Ile Asp

465

470

475

480

Pro Lys Asp Ala Asn Lys Gly Thr Pro Glu Glu Thr Gly Ser Tyr Leu

485

490

495

Val Ser Lys Asp Leu Pro Lys His Cys Leu Tyr Thr Arg Leu Ser Ser

500

505

510

Leu Gln Lys Leu Lys Glu His Leu Val Phe Thr Val Cys Leu Ser Tyr

515

520

525

Gln Tyr Ser Gly Leu Glu Asp Thr Val Glu Asp Lys Gln Glu Val Asn

530

535

540

Val Gly Lys Pro Leu Ile Ala Lys Leu Asp Met His Arg Gly Leu Gly

545

550

555

560

Arg Lys Thr Cys Phe Gln Thr Cys Leu Met Ser Asn Gly Pro Tyr Gln

565

570

575

Ser Ser Ala Ala Thr Ser Gly Gly Ala Gly His Tyr His Ser Leu Gln

580

585

590

Asp Pro Phe His Gly Val Tyr His Ser His Pro Gly Asn Pro Ser Asn

595

600

605

Val Thr Pro Ala Asp Ser Cys His Cys Ser Arg Thr Pro Asp Ala Phe

610

615

620

Ile Ser Ser Phe Ala His His Ala Ser Cys His Phe Ser Arg Ser Asn

625

630

635

640

Val Pro Val Glu Thr Thr Asp Glu Ile Pro Phe Ser Phe Ser Asp Arg

645

650

655

Leu Arg Ile Ser Glu Lys

660

<210> 130

<211> 2251

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (74).. (2059)

<400> 130

cttggctgga cagtttgtga aactgtgttg ccgggcaact ggacatcett ttgttcaata 60

tcagtgggttc aaa atg aat aaa gag att cca aat gga aat aca tca gag 109

457/735

Met Asn Lys Glu Ile Pro Asn Gly Asn Thr Ser Glu

1

5

10

ctt att ttt aat gca gtg cat gta aaa gat gca ggc ttt tat gtc tgt 157

Leu Ile Phe Asn Ala Val His Val Lys Asp Ala Gly Phe Tyr Val Cys

15

20

25

cga gtt aat aac aat ttc acc ttt gaa ttc agc cag tgg tca cag ctg 205

Arg Val Asn Asn Asn Phe Thr Phe Glu Phe Ser Gln Trp Ser Gln Leu

30

35

40

gat gtt tgc gac atc cca gag agc ttc cag aga agt gtt gat ggc gtc 253

Asp Val Cys Asp Ile Pro Glu Ser Phe Gln Arg Ser Val Asp Gly Val

45

50

55

60

tct gaa tcc aag ttg caa atc tgt gtt gaa cca act tcc caa aag ctg 301

Ser Glu Ser Lys Leu Gln Ile Cys Val Glu Pro Thr Ser Gln Lys Leu

65

70

75

atg cca ggc agc aca ttg gtt tta cag tgt gtt gct gtt gga agc cct 349

Met Pro Gly Ser Thr Leu Val Leu Gln Cys Val Ala Val Gly Ser Pro

80

85

90

att cct cac tac cag tgg ttc aaa aat gaa tta cca tta aca cat gag 397

Ile Pro His Tyr Gln Trp Phe Lys Asn Glu Leu Pro Leu Thr His Glu

95

100

105

acc aaa aag cta tac atg gtg cct tat gtg gat ttg gaa cac caa gga 445

Thr Lys Lys Leu Tyr Met Val Pro Tyr Val Asp Leu Glu His Gln Gly

tta ctc ctt tta gac aag gga gta tat ggg tta tta tat tat gca gga 829

Leu Leu Leu Leu Asp Lys Gly Val Tyr Gly Leu Leu Tyr Tyr Ala Gly

240

245

250

cat ggt tat gaa aat ttt ggg aac agc ttc atg gtc ccc gtt gat gct 877

His Gly Tyr Glu Asn Phe Gly Asn Ser Phe Met Val Pro Val Asp Ala

255

260

265

cca aat cca tat agg tct gaa aat tgt ctg tgt gta caa aat ata ctg 925

Pro Asn Pro Tyr Arg Ser Glu Asn Cys Leu Cys Val Gln Asn Ile Leu

270

275

280

aaa ttg atg caa gaa aaa gaa act gga ctt aat gtg ttc tta ttg gat 973

Lys Leu Met Gln Glu Lys Glu Thr Gly Leu Asn Val Phe Leu Leu Asp

285

290

295

300

atg tgt agg aaa aga aat gac tac gat gat acc att cca atc ttg gat 1021

Met Cys Arg Lys Arg Asn Asp Tyr Asp Asp Thr Ile Pro Ile Leu Asp

305

310

315

gca cta aaa gtc acc gcc aat att gtg ttt gga tat gcc acg tgt caa 1069

Ala Leu Lys Val Thr Ala Asn Ile Val Phe Gly Tyr Ala Thr Cys Gln

320

325

330

gga gca gaa gct ttt gaa atc cag cat tct gga ttg gca aat gga atc 1117

Gly Ala Glu Ala Phe Glu Ile Gln His Ser Gly Leu Ala Asn Gly Ile

335

340

345

ttt atg aaa ttt tta aaa gac aga tta tta gaa gat aag aaa atc act 1165

Phe Met Lys Phe Leu Lys Asp Arg Leu Leu Glu Asp Lys Lys Ile Thr

350

355

360

gtg tta ctg gat gaa gtt gca gaa gat atg ggt aag tgt cac ctt acc 1213

Val Leu Leu Asp Glu Val Ala Glu Asp Met Gly Lys Cys His Leu Thr

365

370

375

380

aaa ggc aaa cag gct cta gag att cga agt agt tta tct gag aag aga 1261

Lys Gly Lys Gln Ala Leu Glu Ile Arg Ser Ser Leu Ser Glu Lys Arg

385

390

395

gca ctt act gat cca ata cag gga aca gaa tat tct gct gaa tct ctt 1309

Ala Leu Thr Asp Pro Ile Gln Gly Thr Glu Tyr Ser Ala Glu Ser Leu

400

405

410

gtg cgg aat cta cag tgg gcc aag gct cat gaa ctt cca gaa agt atg 1357

Val Arg Asn Leu Gln Trp Ala Lys Ala His Glu Leu Pro Glu Ser Met

415

420

425

tgt ctt aag ttt gac tgt ggt gtt cag att caa tta gga ttt gca gct 1405

Cys Leu Lys Phe Asp Cys Gly Val Gln Ile Gln Leu Gly Phe Ala Ala

430

435

440

gag ttt tcc aat gtc atg atc atc tat aca agt ata gtt tac aaa cca 1453

Glu Phe Ser Asn Val Met Ile Ile Tyr Thr Ser Ile Val Tyr Lys Pro

445

450

455

460

ccg gag ata ata atg tgt gat gcc tac gtt act gat ttt cca ctt gat 1501

Pro Glu Ile Ile Met Cys Asp Ala Tyr Val Thr Asp Phe Pro Leu Asp

465

470

475

cta gat att gat cca aaa gat gca aat aaa ggc aca cct gaa gaa act 1549

Leu Asp Ile Asp Pro Lys Asp Ala Asn Lys Gly Thr Pro Glu Glu Thr

480

485

490

ggc agc tac ttg gta tca aag gat ctt ccc aag cat tgc ctc tat acc 1597

Gly Ser Tyr Leu Val Ser Lys Asp Leu Pro Lys His Cys Leu Tyr Thr

495

500

505

aga ctc agt tca ctg caa aaa tta aag gaa cat cta gtc ttc aca gta 1645

Arg Leu Ser Ser Leu Gln Lys Leu Lys Glu His Leu Val Phe Thr Val

510

515

520

tgt tta tca tat cag tac tca gga ttg gaa gat act gta gag gac aag 1693

Cys Leu Ser Tyr Gln Tyr Ser Gly Leu Glu Asp Thr Val Glu Asp Lys

525

530

535

540

cag gaa gtg aat gtt ggg aaa cct ctc att gct aaa tta gac atg cat 1741

Gln Glu Val Asn Val Gly Lys Pro Leu Ile Ala Lys Leu Asp Met His

545

550

555

cga ggt ttg gga agg aag act tgc ttt caa act tgt ctt atg tct aat 1789

Arg Gly Leu Gly Arg Lys Thr Cys Phe Gln Thr Cys Leu Met Ser Asn

560

565

570

ggt cct tac cag agt tct gca gcc acc tca gga gga gca ggg cat tat 1837

Gly Pro Tyr Gln Ser Ser Ala Ala Thr Ser Gly Gly Ala Gly His Tyr

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575

580

585

cac tca ttg caa gac cca ttc cat ggt gtt tac cat tca cat cct ggt 1885

His Ser Leu Gln Asp Pro Phe His Gly Val Tyr His Ser His Pro Gly

590

595

600

aat cca agt aat gtt aca cca gca gat agc tgt cat tgc agc cgg act 1933

Asn Pro Ser Asn Val Thr Pro Ala Asp Ser Cys His Cys Ser Arg Thr

605

610

615

620

cca gat gca ttt att tca agt ttc gct cac cat gct tca tgt cat ttt 1981

Pro Asp Ala Phe Ile Ser Ser Phe Ala His His Ala Ser Cys His Phe

625

630

635

agt aga agt aat gtg cca gta gag aca act gat gaa ata cca ttt agt 2029

Ser Arg Ser Asn Val Pro Val Glu Thr Thr Asp Glu Ile Pro Phe Ser

640

645

650

ttc tct gac agg ctc aga att tct gaa aaa tgacctcctt gtttttgaaa 2079

Phe Ser Asp Arg Leu Arg Ile Ser Glu Lys

655

660

gtagcataa ttttagatgc ctgtgaaata gtactgcact tacataaagt gagacattgt 2139

gaaaaggcaa atttgtatat gtagagaaag aatagtagta actgtttcat agcaaacttc 2199

aggactttga gatgttgaaa ttacattatt taattacaga ctctctcttt ct 2251

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Ile Thr Val Asn Pro Glu Ser Lys Ala Val Leu Ala Gly Gln Phe Val

130 135 140

Lys Leu Cys Cys Arg Ala Thr Gly His Pro Phe Val Gln Tyr Gln Trp

145 150 155 160

Phe Lys Met Asn Lys Glu Ile Pro Asn Gly Asn Thr Ser Glu Leu Ile

165 170 175

Phe Asn Ala Val His Val Lys Asp Ala Gly Phe Tyr Val Cys Arg Val

180 185 190

Asn Asn Asn Phe Thr Phe Glu Phe Ser Gln Trp Ser Gln Leu Asp Val

195 200 205

Cys Asp Ile Pro Glu Ser Phe Gln Arg Ser Val Asp Gly Val Ser Glu

210 215 220

Ser Lys Leu Gln Ile Cys Val Glu Pro Thr Ser Gln Lys Leu Met Pro

225 230 235 240

Gly Ser Thr Leu Val Leu Gln Cys Val Ala Val Gly Ser Pro Ile Pro

245 250 255

His Tyr Gln Trp Phe Lys Asn Glu Leu Pro Leu Thr His Glu Thr Lys

260 265 270

Lys Leu Tyr Met Val Pro Tyr Val Asp Leu Glu His Gln Gly Thr Tyr

[illegible]

440

445

450

455

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470

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485

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495

500

505

510

515

520

525

530

535

540

545

550

555

560

565

570

575

580

585

590

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Lys Phe Asp Cys Gly Val Gln Ile Gln Leu Gly Phe Ala Ala Glu Phe

595

600

605

Ser Asn Val Met Ile Ile Tyr Thr Ser Ile Val Tyr Lys Pro Pro Glu

610

615

620

Ile Ile Met Cys Asp Ala Tyr Val Thr Asp Phe Pro Leu Asp Leu Asp

625

630

635

640

Ile Asp Pro Lys Asp Ala Asn Lys Gly Thr Pro Glu Glu Thr Gly Ser

645

650

655

Tyr Leu Val Ser Lys Asp Leu Pro Lys His Cys Leu Tyr Thr Arg Leu

660

665

670

Ser Ser Leu Gln Lys Leu Lys Glu His Leu Val Phe Thr Val Cys Leu

675

680

685

Ser Tyr Gln Tyr Ser Gly Leu Glu Asp Thr Val Glu Asp Lys Gln Glu

690

695

700

Val Asn Val Gly Lys Pro Leu Ile Ala Lys Leu Asp Met His Arg Gly

705

710

715

720

Leu Gly Arg Lys Thr Cys Phe Gln Thr Cys Leu Met Ser Asn Gly Pro

725

730

735

Tyr Gln Ser Ser Ala Ala Thr Ser Gly Gly Ala Gly His Tyr His Ser

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Met Ser Leu Leu

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85 90 95 100

tgc aca gtc aca gaa ttg agt gat ttc ctg cag gct atg gaa cac act 512

Cys Thr Val Thr Glu Leu Ser Asp Phe Leu Gln Ala Met Glu His Thr

105 110 115

gaa gtt ctt cag ctt ctc agc ccc cca gga ata aag att act gta aac 560

Glu Val Leu Gln Leu Leu Ser Pro Pro Gly Ile Lys Ile Thr Val Asn

120 125 130

cca gag tca aag gca gtc ttg gct gga cag ttt gtg aaa ctg tgt tgc 608

Pro Glu Ser Lys Ala Val Leu Ala Gly Gln Phe Val Lys Leu Cys Cys

135 140 145

cgg gca act gga cat cct ttt gtt caa tat cag tgg ttc aaa atg aat 656

Arg Ala Thr Gly His Pro Phe Val Gln Tyr Gln Trp Phe Lys Met Asn

150 155 160

aaa gag att cca aat gga aat aca tca gag ctt att ttt aat gca gtg 704

Lys Glu Ile Pro Asn Gly Asn Thr Ser Glu Leu Ile Phe Asn Ala Val

165 170 175 180

cat gta aaa gat gca ggc ttt tat gtc tgt cga gtt aat aac aat ttc 752

His Val Lys Asp Ala Gly Phe Tyr Val Cys Arg Val Asn Asn Asn Phe

185 190 195

acc ttt gaa ttc agc cag tgg tca cag ctg gat gtt tgc gac atc cca 800

Thr Phe Glu Phe Ser Gln Trp Ser Gln Leu Asp Val Cys Asp Ile Pro

200 205 210

gag agc ttc cag aga agt gtt gat ggc gtc tct gaa tcc aag ttg caa 848

Glu Ser Phe Gln Arg Ser Val Asp Gly Val Ser Glu Ser Lys Leu Gln

215

220

225

atc tgt gtt gaa cca act tcc caa aag ctg atg cca ggc agc aca ttg 896

Ile Cys Val Glu Pro Thr Ser Gln Lys Leu Met Pro Gly Ser Thr Leu

230

235

240

gtt tta cag tgt gtt gct gtt gga agc cct att cct cac tac cag tgg 944

Val Leu Gln Cys Val Ala Val Gly Ser Pro Ile Pro His Tyr Gln Trp

245

250

255

260

ttc aaa aat gaa tta cca tta aca cat gag acc aaa aag cta tac atg 992

Phe Lys Asn Glu Leu Pro Leu Thr His Glu Thr Lys Lys Leu Tyr Met

265

270

275

gtg cct tat gtg gat ttg gaa cac caa gga acc tac tgg tgt cat gta 1040

Val Pro Tyr Val Asp Leu Glu His Gln Gly Thr Tyr Trp Cys His Val

280

285

290

tat aat gat cga gac agt caa gat agc aag aag gta gaa atc atc ata 1088

Tyr Asn Asp Arg Asp Ser Gln Asp Ser Lys Lys Val Glu Ile Ile Ile

295

300

305

gga aga aca gat gag gca gtg gag tgc act gaa gat gaa tta aat aat 1136

Gly Arg Thr Asp Glu Ala Val Glu Cys Thr Glu Asp Glu Leu Asn Asn

310

315

320

ctt ggt cat cct gat aat aaa gag caa aca act gac cag cct ttg gcg 1184

Leu Gly His Pro Asp Asn Lys Glu Gln Thr Thr Asp Gln Pro Leu Ala

325 330 335 340

aag gac aag gtt gcc ctt ttg ata gga aat atg aat tac cgg gag cac 1232

Lys Asp Lys Val Ala Leu Leu Ile Gly Asn Met Asn Tyr Arg Glu His

345 350 355

ccc aag ctc aaa gct cct ttg gtg gat gtg tac gaa ttg act aac tta 1280

Pro Lys Leu Lys Ala Pro Leu Val Asp Val Tyr Glu Leu Thr Asn Leu

360 365 370

ctg aga cag ctg gac ttc aaa gtg gtt tca ctg ttg gat ctt act gaa 1328

Leu Arg Gln Leu Asp Phe Lys Val Val Ser Leu Leu Asp Leu Thr Glu

375 380 385

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Tyr Glu Met Arg Asn Ala Val Asp Glu Phe Leu Leu Leu Leu Asp Lys

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Gly Val Tyr Gly Leu Leu Tyr Tyr Ala Gly His Gly Tyr Glu Asn Phe

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Asp Tyr Asp Asp Thr Ile Pro Ile Leu Asp Ala Leu Lys Val Thr Ala

470

475

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aat att gtg ttt gga tat gcc acg tgt caa gga gca gaa gct ttt gaa 1664

Asn Ile Val Phe Gly Tyr Ala Thr Cys Gln Gly Ala Glu Ala Phe Glu

485

490

495

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atc cag cat tct gga ttg gca aat gga atc ttt atg aaa ttt tta aaa 1712

Ile Gln His Ser Gly Leu Ala Asn Gly Ile Phe Met Lys Phe Leu Lys

505

510

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gac aga tta tta gaa gat aag aaa atc act gtg tta ctg gat gaa gtt 1760

Asp Arg Leu Leu Glu Asp Lys Lys Ile Thr Val Leu Leu Asp Glu Val

520

525

530

gca gaa gat atg ggt aag tgt cac ctt acc aaa ggc aaa cag gct cta 1808

Ala Glu Asp Met Gly Lys Cys His Leu Thr Lys Gly Lys Gln Ala Leu

535

540

545

gag att cga agt agt tta tct gag aag aga gca ctt act gat cca ata 1856

Glu Ile Arg Ser Ser Leu Ser Glu Lys Arg Ala Leu Thr Asp Pro Ile

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550

555

560

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Gln Gly Thr Glu Tyr Ser Ala Glu Ser Leu Val Arg Asn Leu Gln Trp

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570

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gcc aag gct cat gaa ctt cca gaa agt atg tgt ctt aag ttt gac tgt 1952

Ala Lys Ala His Glu Leu Pro Glu Ser Met Cys Leu Lys Phe Asp Cys

585

590

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ggt gtt cag att caa tta gga ttt gca gct gag ttt tcc aat gtc atg 2000

Gly Val Gln Ile Gln Leu Gly Phe Ala Ala Glu Phe Ser Asn Val Met

600

605

610

atc atc tat aca agt ata gtt tac aaa cca ccg gag ata ata atg tgt 2048

Ile Ile Tyr Thr Ser Ile Val Tyr Lys Pro Pro Glu Ile Ile Met Cys

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620

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gat gcc tac gtt act gat ttt cca ctt gat cta gat att gat cca aaa 2096

Asp Ala Tyr Val Thr Asp Phe Pro Leu Asp Leu Asp Ile Asp Pro Lys

630

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640

gat gca aat aaa ggc aca cct gaa gaa act ggc agc tac ttg gta tca 2144

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645

650

655

660

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665

670

675

aaa tta aag gaa cat cta gtc ttc aca gta tgt tta tca tat cag tac 2240

Lys Leu Lys Glu His Leu Val Phe Thr Val Cys Leu Ser Tyr Gln Tyr

680

685

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tca gga ttg gaa gat act gta gag gac aag cag gaa gtg aat gtt ggg 2288

Ser Gly Leu Glu Asp Thr Val Glu Asp Lys Gln Glu Val Asn Val Gly

695

700

705

aaa cct ctc att gct aaa tta gac atg cat cga ggt ttg gga agg aag 2336

Lys Pro Leu Ile Ala Lys Leu Asp Met His Arg Gly Leu Gly Arg Lys

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715

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act tgc ttt caa act tgt ctt atg tct aat ggt cct tac cag agt tct 2384

Thr Cys Phe Gln Thr Cys Leu Met Ser Asn Gly Pro Tyr Gln Ser Ser

725

730

735

740

gca gcc acc tca gga gga gca ggg cat tat cac tca ttg caa gac cca 2432

Ala Ala Thr Ser Gly Gly Ala Gly His Tyr His Ser Leu Gln Asp Pro

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750

755

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Phe His Gly Val Tyr His Ser His Pro Gly Asn Pro Ser Asn Val Thr

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765

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Pro Ala Asp Ser Cys His Cys Ser Arg Thr Pro Asp Ala Phe Ile Ser

775

780

785

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Ser Phe Ala His His Ala Ser Cys His Phe Ser Arg Ser Asn Val Pro
790 795 800

gta gag aca act gat gaa ata cca ttt agt ttc tct gac agg ctc aga 2624
Val Glu Thr Thr Asp Glu Ile Pro Phe Ser Phe Ser Asp Arg Leu Arg
805 810 815 820

att tct gaa aaa tgacctcctt gtttttgaaa gttagcataa ttttagatgc 2676
Ile Ser Glu Lys

ctgtgaaata gtactgcact tacataaagt gagacattgt gaaaaggcaa atttgtatat 2736

gtagagaaag aatagtagta actgtttcat agcaaacttc aggactttga gatgttgaaa 2796

ttacattatt taattacaga cttcctcttt ct 2828

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- <211> 919
- <212> PRT
- <213> Homo sapiens

<400> 133
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Met Ile Pro Val Leu Thr Ser Lys Lys Ala Ser Glu Leu Pro Val Ser
20 25 30

Glu Val Ala Ser Ile Leu Gln Ala Asp Leu Gln Asn Gly Leu Asn Lys

35

40

45

Cys Glu Val Ser His Arg Arg Ala Phe His Gly Trp Asn Glu Phe Asp

50

55

60

Ile Ser Glu Asp Glu Pro Leu Trp Lys Lys Tyr Ile Ser Gln Phe Lys

65

70

75

80

Asn Pro Leu Ile Met Leu Leu Leu Ala Ser Ala Val Ile Ser Val Leu

85

90

95

Met His Gln Phe Asp Asp Ala Val Ser Ile Thr Val Ala Ile Leu Ile

100

105

110

Val Val Thr Val Ala Phe Val Gln Glu Tyr Arg Ser Glu Lys Ser Leu

115

120

125

Glu Glu Leu Ser Lys Leu Val Pro Pro Glu Cys His Cys Val Arg Glu

130

135

140

Gly Lys Leu Glu His Thr Leu Ala Arg Asp Leu Val Pro Gly Asp Thr

145

150

155

160

Val Cys Leu Ser Val Gly Asp Arg Val Pro Ala Asp Leu Arg Leu Phe

165

170

175

Glu Ala Val Asp Leu Ser Ile Asp Glu Ser Ser Leu Thr Gly Glu Thr

[illegible]

345

350

360

365

[illegible]

375

380

385

390

395

400

405

410

415

420

425

430

435

440

445

450

455

460

465

470

475

480

485

490

495

480/735

Asn Val Ile Thr Pro Arg Asp Thr Thr Met Thr Phe Thr Cys Phe Val

805

810

815

Phe Phe Asp Met Phe Asn Ala Leu Ser Ser Arg Ser Gln Thr Lys Ser

820

825

830

Val Phe Glu Ile Gly Leu Cys Ser Asn Arg Met Phe Cys Tyr Ala Val

835

840

845

Leu Gly Ser Ile Met Gly Gln Leu Leu Val Ile Tyr Phe Pro Pro Leu

850

855

860

Gln Lys Val Phe Gln Thr Glu Ser Leu Ser Ile Leu Asp Leu Leu Phe

865

870

875

880

Leu Leu Gly Leu Thr Ser Ser Val Cys Ile Val Ala Glu Ile Ile Lys

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890

895

Lys Val Glu Arg Ser Arg Glu Lys Ile Gln Lys His Val Ser Ser Thr

900

905

910

Ser Ser Ser Phe Leu Glu Val

915

<210> 134

<211> 3612

<212> DNA

<213> Homo sapiens

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Figure 1 is a line graph illustrating the percentage of the total sample for each age group across different years. The y-axis represents the percentage of the total sample, ranging from 0 to 100. The x-axis represents the years (1970, 1980, 1990, 2000, 2010, 2020). The graph shows a clear trend of aging, with the 0-14 age group decreasing from approximately 25% in 1970 to 10% in 2020, and the 65-74 age group increasing from approximately 10% in 1970 to 25% in 2020.

cctccccgcc cgccctctct cctcccttc cteccctccg ctcgcttett ctcacgccgg 120

ggggcgcccc cgcgagcccc gcggctgaga cccgcagcc tggaggaggg ctgtccgggg 240

ggtgacagcc tgggattccg ggggcttctc ttccttgtec tcctcctctc ctctctattc 360

tgga aa atg aag gtt gca cgt ttt caa aaa ata cct aat ggt gaa aat 468

gag aca atg att cct gta ttg aca tca aaa aaa gca agt gaa tta cca 516

15 20 25 30

484/735

485/735

145

150

155

gat aca gtt tgc ctt tct gtt ggg gat aga gtt cct gct gac tta cgc 948

Asp Thr Val Cys Leu Ser Val Gly Asp Arg Val Pro Ala Asp Leu Arg

160

165

170

ttg ttt gag gct gtg gat ctt tcc att gat gag tcc agc ttg aca ggt 996

Leu Phe Glu Ala Val Asp Leu Ser Ile Asp Glu Ser Ser Leu Thr Gly

175

180

185

190

gag aca acg cct tgt tct aag gtg aca gct cct cag cca gct gca act 1044

Glu Thr Thr Pro Cys Ser Lys Val Thr Ala Pro Gln Pro Ala Ala Thr

195

200

205

aat gga gat ctt gca tcg aga agt aac att gcc ttt atg gga aca ctg 1092

Asn Gly Asp Leu Ala Ser Arg Ser Asn Ile Ala Phe Met Gly Thr Leu

210

215

220

gtc aga tgt ggc aaa gca aag ggt gtt gtc att gga aca gga gaa aat 1140

Val Arg Cys Gly Lys Ala Lys Gly Val Val Ile Gly Thr Gly Glu Asn

225

230

235

tct gaa ttt ggg gag gtt ttt aaa atg atg caa gca gaa gag gca cca 1188

Ser Glu Phe Gly Glu Val Phe Lys Met Met Gln Ala Glu Glu Ala Pro

240

245

250

aaa acc cct ctg cag aag agc atg gac ctc tta gga aaa caa ctt tcc 1236

Lys Thr Pro Leu Gln Lys Ser Met Asp Leu Leu Gly Lys Gln Leu Ser

255

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270

ttt tac tcc ttt ggt ata ata gga atc atc atg ttg gtt ggc tgg tta 1284

Phe Tyr Ser Phe Gly Ile Ile Gly Ile Ile Met Leu Val Gly Trp Leu

275

280

285

ctg gga aaa gat atc ctg gaa atg ttt act att agt gta agt ttg gct 1332

Leu Gly Lys Asp Ile Leu Glu Met Phe Thr Ile Ser Val Ser Leu Ala

290

295

300

gta gca gca att cct gaa ggt ctc ccc att gtg gtc aca gtg acg cta 1380

Val Ala Ala Ile Pro Glu Gly Leu Pro Ile Val Val Thr Val Thr Leu

305

310

315

gct ctt ggt gtt atg aga atg gtg aag aaa agg gcc att gtg aaa aag 1428

Ala Leu Gly Val Met Arg Met Val Lys Lys Arg Ala Ile Val Lys Lys

320

325

330

ctg cct att gtt gaa act ctg ggc tgc tgt aat gtg att tgt tca gat 1476

Leu Pro Ile Val Glu Thr Leu Gly Cys Cys Asn Val Ile Cys Ser Asp

335

340

345

350

aaa act gga aca ctg acg aag aat gaa atg act gtt act cac ata ttt 1524

Lys Thr Gly Thr Leu Thr Lys Asn Glu Met Thr Val Thr His Ile Phe

355

360

365

act tca gat ggt ctg cat gct gag gtt act gga gtt ggc tat aat caa 1572

Thr Ser Asp Gly Leu His Ala Glu Val Thr Gly Val Gly Tyr Asn Gln

370

375

380

ttt ggg gaa gtg att gtt gat ggt gat gtt gtt cat gga ttc tat aac 1620

Phe Gly Glu Val Ile Val Asp Gly Asp Val Val His Gly Phe Tyr Asn

385

390

395

cca gct gtt agc aga att gtt gag gcg ggc tgt gtg tgc aat gat gct 1668

Pro Ala Val Ser Arg Ile Val Glu Ala Gly Cys Val Cys Asn Asp Ala

400

405

410

gta att aga aac aat act cta atg ggg aag cca aca gaa ggg gcc tta 1716

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415

420

425

430

att gct ctt gca atg aag atg ggt ctt gat gga ctt caa caa gac tac 1764

Ile Ala Leu Ala Met Lys Met Gly Leu Asp Gly Leu Gln Gln Asp Tyr

435

440

445

atc aga aaa gct gaa tac cct ttt agc tct gag caa aag tgg atg gct 1812

Ile Arg Lys Ala Glu Tyr Pro Phe Ser Ser Glu Gln Lys Trp Met Ala

450

455

460

gtt aag tgt gta cac cga aca cag cag gac aga cca gag att tgt ttt 1860

Val Lys Cys Val His Arg Thr Gln Gln Asp Arg Pro Glu Ile Cys Phe

465

470

475

atg aaa ggt gct tac gaa caa gta att aag tac tgt act aca tac cag 1908

Met Lys Gly Ala Tyr Glu Gln Val Ile Lys Tyr Cys Thr Thr Tyr Gln

480

485

490

agc aaa ggg cag acc ttg aca ctt act cag cag cag aga gat gtg tac 1956

488/735

Ser Lys Gly Gln Thr Leu Thr Leu Thr Gln Gln Gln Arg Asp Val Tyr

495 500 505 510

caa caa gag aag gca cgc atg ggc tca gcg gga ctc aga gtt ctt gct 2004

Gln Gln Glu Lys Ala Arg Met Gly Ser Ala Gly Leu Arg Val Leu Ala

515 520 525

ttg gct tct ggt cct gaa ctg gga cag ctg aca ttt ctt ggc ttg gtg 2052

Leu Ala Ser Gly Pro Glu Leu Gly Gln Leu Thr Phe Leu Gly Leu Val

530 535 540

gga atc att gat cca cct aga act ggt gtg aaa gaa gct gtt aca aca 2100

Gly Ile Ile Asp Pro Pro Arg Thr Gly Val Lys Glu Ala Val Thr Thr

545 550 555

ctc att gcc tca gga gta tca ata aaa atg att act gga gat tca cag 2148

Leu Ile Ala Ser Gly Val Ser Ile Lys Met Ile Thr Gly Asp Ser Gln

560 565 570

gag act gca gtt gca atc gcc agt cgt ctg gga ttg tat tcc aaa act 2196

Glu Thr Ala Val Ala Ile Ala Ser Arg Leu Gly Leu Tyr Ser Lys Thr

575 580 585 590

tcc cag tca gtc tca gga gaa gaa ata gat gca atg gat gtt cag cag 2244

Ser Gln Ser Val Ser Gly Glu Glu Ile Asp Ala Met Asp Val Gln Gln

595 600 605

ctt tca caa ata gta cca aag gtt gca gta ttt tac aga gct agc cca 2292

Leu Ser Gln Ile Val Pro Lys Val Ala Val Phe Tyr Arg Ala Ser Pro

610

615

620

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Arg His Lys Met Lys Ile Ile Lys Ser Leu Gln Lys Asn Gly Ser Val

625

630

635

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640

645

650

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655

660

665

670

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675

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685

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Ser Ala Ile Glu Glu Gly Lys Gly Ile Tyr Asn Asn Ile Lys Asn Phe

690

695

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710

715

ttg gct aca tta atg aac ttt cct aat cct ctc aat gcc atg cag att 2628
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720

725

730

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735 740 745 750

gta gaa cca gtg gat aaa gat gtc att cgt aaa cct cct cgc aac tgg 2724
Val Glu Pro Val Asp Lys Asp Val Ile Arg Lys Pro Pro Arg Asn Trp
755 760 765

aaa gac agc att ttg act aaa aac ttg ata ctt aaa ata ctt gtt tca 2772
Lys Asp Ser Ile Leu Thr Lys Asn Leu Ile Leu Lys Ile Leu Val Ser
770 775 780

tca ata atc att gtt tgt ggg act ttg ttt gtc ttc tgg cgt gag cta 2820
Ser Ile Ile Ile Val Cys Gly Thr Leu Phe Val Phe Trp Arg Glu Leu
785 790 795

cga gac aat gtg att aca cct cga gac aca aca atg acc ttc aca tgc 2868
Arg Asp Asn Val Ile Thr Pro Arg Asp Thr Thr Met Thr Phe Thr Cys
800 805 810

ttt gtg ttt ttt gac atg ttc aat gca cta agt tcc aga tcc cag acc 2916
Phe Val Phe Phe Asp Met Phe Asn Ala Leu Ser Ser Arg Ser Gln Thr
815 820 825 830

aag tct gtg ttt gag att gga ctc tgc agt aat aga atg ttt tgc tat 2964
Lys Ser Val Phe Glu Ile Gly Leu Cys Ser Asn Arg Met Phe Cys Tyr
835 840 845

gca gtt ctt gga tcc atc atg gga caa tta cta gtt att tac ttt cct 3012

Ala Val Leu Gly Ser Ile Met Gly Gln Leu Leu Val Ile Tyr Phe Pro

850 855 860

ccg ctt cag aag gtt ttt cag act gag agc cta agc ata ctg gat ctg 3060

Pro Leu Gln Lys Val Phe Gln Thr Glu Ser Leu Ser Ile Leu Asp Leu

865 870 875

ttg ttt ctt ttg ggt ctc acc tca tca gtg tgc ata gtg gca gaa att 3108

Leu Phe Leu Leu Gly Leu Thr Ser Ser Val Cys Ile Val Ala Glu Ile

880 885 890

ata aag aag gtt gaa agg agc agg gaa aag atc cag aag cat gtt agt 3156

Ile Lys Lys Val Glu Arg Ser Arg Glu Lys Ile Gln Lys His Val Ser

895 900 905 910

tcg aca tca tca tct ttt ctt gaa gta tgatgcatat tgcattattt 3203

Ser Thr Ser Ser Ser Phe Leu Glu Val

915

tatttgcaaa ctaggaattg cagtctgagg atcatttaga agggcaagtt caagaggata 3263

tgaagatttg agaacttttt aactattcat tgactaaaaa tgaacattaa tgttaaagac 3323

ttaagacttt aacctgctgg cagtcccaaa tgaaattatg caactttgat atcatattcc 3383

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aattaaaaag gcaaaacctg aaccaccttc tgcacttaaa gaagtctaac agtacaaata 3503

[illegible][illegible][illegible]

Figure 1 is a line graph showing the effect of the concentration of the inhibitor on the rate of polymerization. The y-axis is labeled $R_p \times 10^4$ and ranges from 0 to 1.0. The x-axis is labeled $C \times 10^2$ and ranges from 0 to 1.0. The curve starts at (0, 1.0) and decreases as C increases, reaching approximately 0.4 at $C = 1.0$. The curve is labeled $R_p \times 10^4$ and $C \times 10^2$.

1

120

180

240

300

360

420

473

473

5

473

521

521

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521

agc agc atg caa ggc tgg cgt gtt gaa atg gag gat gca cat acg gct 569

Ser Ser Met Gln Gly Trp Arg Val Glu Met Glu Asp Ala His Thr Ala

30

35

40

gtg atc ggt ttg cca agt gga ctt gaa tcg tgg tca ttc ttt gct gtg 617

Val Ile Gly Leu Pro Ser Gly Leu Glu Ser Trp Ser Phe Phe Ala Val

45

50

55

tat gat ggg cat gct ggt tct cag gtt gcc aaa tac tgc tgt gag cat 665

Tyr Asp Gly His Ala Gly Ser Gln Val Ala Lys Tyr Cys Cys Glu His

60

65

70

ttg tta gat cac atc acc aat aac cag gat ttt aaa ggg tct gca gga 713

Leu Leu Asp His Ile Thr Asn Asn Gln Asp Phe Lys Gly Ser Ala Gly

75

80

85

90

gca cct tct gtg gaa aat gta aag aat gga atc aga aca ggt ttt ctg 761

Ala Pro Ser Val Glu Asn Val Lys Asn Gly Ile Arg Thr Gly Phe Leu

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100

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110

115

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125

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Thr Tyr Phe Ile Asn Cys Gly Asp Ser Arg Gly Leu Leu Cys Arg Asn
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Arg Lys Val His Phe Phe Thr Gln Asp His Lys Pro Ser Asn Pro Leu
155 160 165 170

gag aaa gaa cga att cag aat gca ggt ggc tct gta atg att cag cgt 1001
Glu Lys Glu Arg Ile Gln Asn Ala Gly Gly Ser Val Met Ile Gln Arg
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Val Asn Gly Ser Leu Ala Val Ser Arg Ala Leu Gly Asp Phe Asp Tyr
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aaa tgt gtc cat gga aaa ggt cct act gag cag ctt gtc tca cca gag 1097
Lys Cys Val His Gly Lys Gly Pro Thr Glu Gln Leu Val Ser Pro Glu
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cct gaa gtc cat gat att gaa aga tct gaa gaa gat gat cag ttc att 1145
Pro Glu Val His Asp Ile Glu Arg Ser Glu Glu Asp Asp Gln Phe Ile
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atc ctt gca tgt gat ggt atc tgg gat gtt atg gga aat gaa gag ctc 1193
Ile Leu Ala Cys Asp Gly Ile Trp Asp Val Met Gly Asn Glu Glu Leu
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tgt gat ttt gta aga tcc aga ctt gaa gtc act gat gac ctt gag aaa 1241
498/735

Cys Asp Phe Val Arg Ser Arg Leu Glu Val Thr Asp Asp Leu Glu Lys

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Pro Gly Gly Glu Leu Ala Ser Lys Arg Asn Val Ile Glu Ala Val Tyr

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Asn Arg Leu Asn Pro Tyr Lys Asn Asp Asp Thr Asp Ser Thr Ser Thr

499/735

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370

375

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Asp Asp Met Trp

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caggtaataa tacagtgtat tcataaga at ctcaatcttg gggctaaatg ccttggtttct 2289

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35 40 45

Thr Leu Phe Val Asn Gly Gln Pro Arg Pro Leu Glu Ser Ser Gln Val

50 55 60

Lys Tyr Leu Arg Arg Glu Leu Ile Glu Leu Arg Asn Lys Val Asn Arg

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Leu Leu Asp Ser Leu Glu Pro Pro Gly Glu Pro Gly Pro Ser Thr Asn

85 90 95

Ile Pro Glu Asn Asp Thr Val Asp Gly Arg Glu Glu Lys Ser Ala Ser
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Asp Ser Ser Gly Lys Gln Ser Thr Gln Val Met Ala Ala Ser Met Ser
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Ala Phe Asp Pro Leu Lys Asn Gln Asp Glu Ile Asn Lys Asn Val Met
130 135 140

Ser Ala Phe Gly Leu Thr Asp Asp Gln Val Ser Gly Pro Pro Ser Ala
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Pro Ala Glu Asp Arg Ser Gly Thr Pro Asp Ser Ile Ala Ser Ser Ser
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Ser Ala Ala His Pro Pro Gly Val Gln Pro Gln Gln Pro Pro Tyr Thr
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Gly Ala Gln Thr Gln Ala Gly Gln Met Tyr Gln Gln Tyr Gln Gln Gln
195 200 205

Ala Gly Tyr Gly Ala Gln Gln Pro Gln Ala Pro Pro Gln Gln Pro Gln
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502/735

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Ser Gln Val Lys Tyr Leu Arg Arg Glu Leu Ile Glu Leu Arg Asn Lys

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Val Asn Arg Leu Leu Asp Ser Leu Glu Pro Pro Gly Glu Pro Gly Pro

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Ser Thr Asn Ile Pro Glu Asn Asp Thr Val Asp Gly Arg Glu Glu Lys

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Ser Met Ser Ala Phe Asp Pro Leu Lys Asn Gln Asp Glu Ile Asn Lys

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ccc agt gct cct gca gaa gat cgt tca gga aca ccc gac agc att gct 529

Pro Ser Ala Pro Ala Glu Asp Arg Ser Gly Thr Pro Asp Ser Ile Ala

160

165

170

tcc tcc tcc tca gca gct cac cca cca ggc gtt cag cca cag cag cca 577

Ser Ser Ser Ser Ala Ala His Pro Pro Gly Val Gln Pro Gln Gln Pro

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cca tat aca gga gct cag act caa gca ggt cag atg tac caa cag tac 625

Pro Tyr Thr Gly Ala Gln Thr Gln Ala Gly Gln Met Tyr Gln Gln Tyr

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Gln Pro Gln Gln Tyr Gly Ile Gln Tyr Ser Ala Ser Tyr Ser Gln Gln

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Pro Ala Gln Pro Pro Gln Gln Tyr Gln Ala Ser Asn Tyr Pro Ala Gln

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gcc tct caa cct gga atg gct cca agc caa cct ggg gcc tat caa cca 961

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Tyr Thr Gln Pro Gly Pro Gly Tyr Arg

350

355

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35 40 45

Leu Ser Asn Asp Glu Val Thr Ile Lys Tyr Lys Asp Glu Asp Gly Asp
50 55 60

Leu Ile Thr Ile Phe Asp Ser Ser Asp Leu Ser Phe Ala Ile Gln Cys
65 70 75 80

Ser Arg Ile Leu Lys Leu Thr Leu Phe Val Asn Gly Gln Pro Arg Pro
85 90 95

Leu Glu Ser Ser Gln Val Lys Tyr Leu Arg Arg Glu Leu Ile Glu Leu
100 105 110

Arg Asn Lys Val Asn Arg Leu Leu Asp Ser Leu Glu Pro Pro Gly Glu
115 120 125

Pro Gly Pro Ser Thr Asn Ile Pro Glu Asn Asp Thr Val Asp Gly Arg
130 135 140

Gln Gln Leu Pro Ala Gln Pro Pro Gln Gln Tyr Gln Ala Ser Asn Tyr

305 310 315 320

Pro Ala Gln Thr Tyr Thr Ala Gln Thr Ser Gln Pro Thr Asn Tyr Thr

325 330 335

Val Ala Pro Ala Ser Gln Pro Gly Met Ala Pro Ser Gln Pro Gly Ala

340 345 350

Tyr Gln Pro Arg Pro Gly Phe Thr Ser Leu Pro Gly Ser Thr Met Thr

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Pro Pro Pro Ser Gly Pro Asn Pro Tyr Ala Arg Asn Arg Pro Pro Phe

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Gly Gln Gly Tyr Thr Gln Pro Gly Pro Gly Tyr Arg

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Ile Val Lys Ala Gln Leu Gly Glu Asp Ile Arg Arg Ile Pro Ile His

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Asn Glu Asp Ile Thr Tyr Asp Glu Leu Val Leu Met Met Gln Arg Val

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Phe Arg Gly Lys Leu Leu Ser Asn Asp Glu Val Thr Ile Lys Tyr Lys

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gat gaa gat gga gat ctt ata aca att ttt gat agt tct gac ctt tcc 243

Asp Glu Asp Gly Asp Leu Ile Thr Ile Phe Asp Ser Ser Asp Leu Ser

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Phe Ala Ile Gln Cys Ser Arg Ile Leu Lys Leu Thr Leu Phe Val Asn

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Gly Gln Pro Arg Pro Leu Glu Ser Ser Gln Val Lys Tyr Leu Arg Arg

95 100 105

gaa ctg ata gaa ctt cga aat aaa gtg aat cgt tta ttg gat agc ttg 387

Glu Leu Ile Glu Leu Arg Asn Lys Val Asn Arg Leu Leu Asp Ser Leu

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Thr Asp Asp Gln Val Ser Gly Pro Pro Ser Ala Pro Ala Glu Asp Arg

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205

210

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Gln Gln Pro Gln Ala Pro Pro Gln Gln Pro Gln Gln Tyr Gly Ile Gln
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Phe Ser Gly Gln Pro Gln Gln Leu Pro Ala Gln Pro Pro Gln Gln Tyr
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320 325 330

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Arg

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Val Pro Phe His Arg Val Asp Thr Ile Ser Val Asn Gly Ser Val Gln

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Leu Ser Tyr Ile Ser Phe Gln Pro Pro Gly Val Trp Pro Ala Asn Pro

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Gln Met Phe Ser Thr Pro Ala Ile Pro Pro Met Met Tyr Pro His Pro

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Ala Tyr Pro Met Pro Phe Ile Thr Thr Ile Leu Gly Gly Leu Tyr Pro

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Ser Lys Ser Ile Leu Leu Ser Gly Thr Val Leu Pro Ser Ala Gln Arg

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215

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ttc cac atc aac ctg tgc tct ggg aac cac atc gcc ttc cac ctg aac 782

Phe His Ile Asn Leu Cys Ser Gly Asn His Ile Ala Phe His Leu Asn

225

230

235

ccc cgt ttt gat gag aat gct gtg gtc cgc aac acc cag atc gac aac 830

Pro Arg Phe Asp Glu Asn Ala Val Val Arg Asn Thr Gln Ile Asp Asn

240

245

250

tcc tgg ggg tct gag gag cga agt ctg ccc cga aaa atg ccc ttc gtc 878

Ser Trp Gly Ser Glu Glu Arg Ser Leu Pro Arg Lys Met Pro Phe Val

255

260

265

cgt ggc cag agc ttc tca gtg tgg atc ttg tgt gaa gct cac tgc ctc 926

Arg Gly Gln Ser Phe Ser Val Trp Ile Leu Cys Glu Ala His Cys Leu

270

275

280

285

aag gtg gcc gtg gat ggt cag cac ctg ttt gaa tac tac cat cgc ctg 974

Lys Val Ala Val Asp Gly Gln His Leu Phe Glu Tyr Tyr His Arg Leu

290

295

300

agg aac ctg ccc acc atc aac aga ctg gaa gtg ggg ggc gac atc cag 1022

Arg Asn Leu Pro Thr Ile Asn Arg Leu Glu Val Gly Gly Asp Ile Gln

305

310

315

ctg acc cat gtg cag aca taggcggctt cctggccctg gggccggggg 1070

Leu Thr His Val Gln Thr

320

ctggggtgtg gggcagtctg ggctctctca tcateccac ttcccaggcc cagcctttcc 1130

aaccctgcct gggatctggg ctttaatgca gaggccatgt ccttgtctgg tctgtcttct 1190

ggctacagcc accctggaac ggagaaggca gctgacgggg attgccttcc tcagccgcag 1250

cagcacctgg ggtccagct gctggaatcc taccatccca ggaggcaggc acagccaggg 1310

agaggggagg agtgggcagt gaagatgaag ccccatgctc agtccccctcc catccccccac 1370

gcagctccac cccagtcacca agccaccagc tgtctgctcc tgggtgggagg tggcctcctc 1430

agccccctct ctctgacett taacctcact ctcaccttgc accgtgcacc aaccttcac 1490

ccctcctgga aagcaggeet gatggettcc cactggcctc caccacctga ccagagtgtt 1550

ctcttcagag gactggctcc tttcccagtg tccttaaaat aaagaaatga aaatgcttgt 1610

tggcac 1616

- <210> 143
- <211> 136
- <212> PRT
- <213> Homo sapiens

<400> 143

Met Ala Gly Ala Ile Ile Glu Asn Met Ser Thr Lys Lys Leu Cys Ile

1 5 10 15

Val Gly Gly Ile Leu Leu Val Phe Gln Ile Ile Ala Phe Leu Val Gly

20 25 30

Gly Leu Ile Ala Pro Gly Pro Thr Thr Ala Val Ser Tyr Met Ser Val

521/735

<400> 144

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cccagaaagg aggcgaggaa ggagggagtg tgtgagagga gggagcaaaa agctcaccct 180

aaaacattta tttcaaggag aaaagaaaaa gggggggcgc aaaa atg gct ggg gca 236

Met Ala Gly Ala

1

att ata gaa aac atg agc acc aag aag ctg tgc att gtt ggt ggg att 284

Ile Ile Glu Asn Met Ser Thr Lys Lys Leu Cys Ile Val Gly Gly Ile

5

10

15

20

ctg etc gtg ttc caa atc atc gcc ttt ctg gtg gga ggc ttg att gct 332

Leu Leu Val Phe Gln Ile Ile Ala Phe Leu Val Gly Gly Leu Ile Ala

25

30

35

cca ggg ccc aca acg gca gtg tcc tac atg tcg gtg aaa tgt gtg gat 380

Pro Gly Pro Thr Thr Ala Val Ser Tyr Met Ser Val Lys Cys Val Asp

40

45

50

gcc cgt aag aac cat cac aag aca aaa tgg ttc gtg cct tgg gga ccc 428

Ala Arg Lys Asn His His Lys Thr Lys Trp Phe Val Pro Trp Gly Pro

55

60

65

aat cat tgt gac aag atc cga gac att gaa gag gca att cca agg gaa 476

523/735

Asn His Cys Asp Lys Ile Arg Asp Ile Glu Glu Ala Ile Pro Arg Glu

70 75 80

att gaa gcc aat gac atc gtg ttt tct gtt cac att ccc ctc ccc cac 524

Ile Glu Ala Asn Asp Ile Val Phe Ser Val His Ile Pro Leu Pro His

85 90 95 100

atg gct ctt agc tgt ggt ttc ttg gac cag cgg cat gga cat ttg tca 572

Met Ala Leu Ser Cys Gly Phe Leu Asp Gln Arg His Gly His Leu Ser

105 110 115

gtt tgc ctt ctg acg gta gct ttt gga gga aga ttc ctg cag cca cta 620

Val Cys Leu Leu Thr Val Ala Phe Gly Gly Arg Phe Leu Gln Pro Leu

120 125 130

atg cat tgt gta tgataacaaa aactctggta tgacacattt tctgtgatca 672

Met His Cys Val

135

ttgttaatta gtgacatagt aacatctgta gcagctgggt agtaaaccctc atgtgggggt 732

ggggtggggg tgtattcctt gggggatggt ttgggccgaa tggggagtgg aatatttgac 792

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atcaccaggt agcctactga gttaatattt aagttgtcaa tagataagtg tccctgtttt 972

Asp Asp Ala Phe Ala Glu Trp Thr Glu Met Ala His Glu Arg Val Pro
65 70 75 80

Arg Lys Leu Lys Cys Thr Phe Thr Ser Pro Lys Thr Pro Glu His Glu
85 90 95

Gly Arg Tyr Tyr Glu Cys Asp Val Leu Pro Phe Met Glu Ile Gly Ser
100 105 110

Val Ala His Lys Phe Tyr Leu Leu Asn Ile Arg Leu Pro Val Asn Glu
115 120 125

Lys Lys Lys Ile Asn Val Gly Ile Gly Glu Ile Lys Asp Ile Arg Leu
130 135 140

Val Gly Ile His Gln Asn Gly Gly Phe Thr Lys Val Trp Phe Ala Met
145 150 155 160

Lys Thr Phe Leu Thr Pro Ser Ile Phe Ile Ile Met Val Trp Tyr Trp
165 170 175

Arg Arg Ile Thr Met Met Ser Arg Pro Pro Val Leu Leu Glu Lys Val
180 185 190

Ile Phe Ala Leu Gly Ile Ser Met Thr Phe Ile Asn Ile Pro Val Glu
195 200 205

Trp Phe Ser Ile Gly Phe Asp Trp Thr Trp Met Leu Leu Phe Gly Asp
210 215 220

Ile Arg Gln Gly Ile Phe Tyr Ala Met Leu Leu Ser Phe Trp Ile Ile
225 230 235 240

Phe Cys Gly Glu His Met Met Asp Gln His Glu Arg Asn His Ile Ala
245 250 255

Gly Tyr Trp Lys Gln Val Gly Pro Ile Ala Val Gly Ser Phe Cys Leu
260 265 270

Phe Ile Phe Asp Met Cys Glu Arg Gly Val Gln Leu Thr Asn Pro Phe
275 280 285

Tyr Ser Ile Trp Thr Thr Asp Ile Gly Thr Glu Leu Ala Met Ala Phe
290 295 300

Ile Ile Val Ala Gly Ile Cys Leu Cys Leu Tyr Phe Leu Phe Leu Cys
305 310 315 320

Phe Met Val Phe Gln Val Phe Arg Asn Ile Ser Gly Lys Gln Ser Ser
325 330 335

Leu Pro Ala Met Ser Lys Val Arg Arg Leu His Tyr Glu Gly Leu Ile
340 345 350

Phe Arg Phe Lys Phe Leu Met Leu Ile Thr Leu Ala Cys Ala Ala Met
355 360 365

Thr Val Ile Phe Phe Ile Val Ser Gln Val Thr Glu Gly His Trp Lys
527/735

370

375

380

Trp Gly Gly Val Thr Val Gln Val Asn Ser Ala Phe Phe Thr Gly Ile

385

390

395

400

Tyr Gly Met Trp Asn Leu Tyr Val Phe Ala Leu Met Phe Leu Tyr Ala

405

410

415

Pro Ser His Lys Asn Tyr Gly Glu Asp Gln Ser Asn Gly Met Gln Leu

420

425

430

Pro Cys Lys Ser Arg Glu Asp Cys Ala Leu Phe Val Ser Glu Leu Tyr

435

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Gln Glu Leu Phe Ser Ala Ser Lys Tyr Ser Phe Ile Asn Asp Asn Ala

450

455

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Ala Ser Gly Ile

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<212> DNA

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<220>

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cccagaaagg aggcgaggaa ggagggagtg tgtgagagga gggagcaaaa agctcaccct 180

aaaacattta tttcaaggag aaaagaaaaa gggggggcgc aaaaatggct ggggcaatta 240

tagaaaacat gaggaccaag aagctgtgca ttgttggtgg gattctgctc gtgttccaaa 300

tcatgcctt tctggtggga ggcttgattg ctccagggcc cacaacggca gtgtcctaca 360

tgtcggtgaa atgtgtgg atg ccc gta aga acc atc aca aga caa aat ggt 411

Met Pro Val Arg Thr Ile Thr Arg Gln Asn Gly

1

5

10

tcg tgc ctt ggg gac cca atc att gtg aca aga tcc gag aca ttg aag 459

Ser Cys Leu Gly Asp Pro Ile Ile Val Thr Arg Ser Glu Thr Leu Lys

15

20

25

agg caa ttc caa ttc atg ctg ttt atc ctg cag ctg gac att gcc ttc 507

Arg Gln Phe Gln Phe Met Leu Phe Ile Leu Gln Leu Asp Ile Ala Phe

30

35

40

aag cta aac aac caa atc aga gaa aat gca gaa gtc tcc atg gac gtt 555

Lys Leu Asn Asn Gln Ile Arg Glu Asn Ala Glu Val Ser Met Asp Val

45

50

55

529/735

tcc ctg gct tac cgt gat gac gcg ttt gct gag tgg act gaa atg gcc 603

Ser Leu Ala Tyr Arg Asp Asp Ala Phe Ala Glu Trp Thr Glu Met Ala

60

65

70

75

cat gaa aga gta cca cgg aaa ctc aaa tgc acc ttc aca tct ccc aag 651

His Glu Arg Val Pro Arg Lys Leu Lys Cys Thr Phe Thr Ser Pro Lys

80

85

90

act cca gag cat gag ggc cgt tac tat gaa tgt gat gtc ctt cct ttc 699

Thr Pro Glu His Glu Gly Arg Tyr Tyr Glu Cys Asp Val Leu Pro Phe

95

100

105

atg gaa att ggg tct gtg gcc cat aag ttt tac ctt tta aac atc cgg 747

Met Glu Ile Gly Ser Val Ala His Lys Phe Tyr Leu Leu Asn Ile Arg

110

115

120

ctg cct gtg aat gag aag aag aaa atc aat gtg gga att ggg gag ata 795

Leu Pro Val Asn Glu Lys Lys Lys Ile Asn Val Gly Ile Gly Glu Ile

125

130

135

aag gat atc cgg ttg gtg ggg atc cac caa aat gga ggc ttc acc aag 843

Lys Asp Ile Arg Leu Val Gly Ile His Gln Asn Gly Gly Phe Thr Lys

140

145

150

155

gtg tgg ttt gcc atg aag acc ttc ctt acg ccc agc atc ttc atc att 891

Val Trp Phe Ala Met Lys Thr Phe Leu Thr Pro Ser Ile Phe Ile Ile

160

165

170

atg gtg tgg tat tgg agg agg atc acc atg atg tcc cga ccc cca gtg 939

Met Val Trp Tyr Trp Arg Arg Ile Thr Met Met Ser Arg Pro Pro Val

175

180

185

ctt ctg gaa aaa gtc atc ttt gcc ctt ggg att tcc atg acc ttt atc 987

Leu Leu Glu Lys Val Ile Phe Ala Leu Gly Ile Ser Met Thr Phe Ile

190

195

200

aat atc cca gtg gaa tgg ttt tcc atc ggg ttt gac tgg acc tgg atg 1035

Asn Ile Pro Val Glu Trp Phe Ser Ile Gly Phe Asp Trp Thr Trp Met

205

210

215

ctg ctg ttt ggt gac atc cga cag ggc atc ttc tat gcg atg ctt ctg 1083

Leu Leu Phe Gly Asp Ile Arg Gln Gly Ile Phe Tyr Ala Met Leu Leu

220

225

230

235

tcc ttc tgg atc atc ttc tgt ggc gag cac atg atg gat cag cac gag 1131

Ser Phe Trp Ile Ile Phe Cys Gly Glu His Met Met Asp Gln His Glu

240

245

250

cgg aac cac atc gca ggg tat tgg aag caa gtc gga ccc att gcc gtt 1179

Arg Asn His Ile Ala Gly Tyr Trp Lys Gln Val Gly Pro Ile Ala Val

255

260

265

ggc tcc ttc tgc ctc ttc ata ttt gac atg tgt gag aga ggg gta caa 1227

Gly Ser Phe Cys Leu Phe Ile Phe Asp Met Cys Glu Arg Gly Val Gln

270

275

280

ctc acg aat ccc ttc tac agt atc tgg act aca gac att gga aca gag 1275

531/735

Leu Thr Asn Pro Phe Tyr Ser Ile Trp Thr Thr Asp Ile Gly Thr Glu
285 290 295

ctg gcc atg gcc ttc atc atc gtg gct gga atc tgc ctc tgc ctc tac 1323
Leu Ala Met Ala Phe Ile Ile Val Ala Gly Ile Cys Leu Cys Leu Tyr
300 305 310 315

ttc ctg ttt cta tgc ttc atg gta ttt cag gtg ttt cgg aac atc agt 1371
Phe Leu Phe Leu Cys Phe Met Val Phe Gln Val Phe Arg Asn Ile Ser
320 325 330

ggg aag cag tcc agc ctg cca gct atg agc aaa gtc cgg cgg cta cac 1419
Gly Lys Gln Ser Ser Leu Pro Ala Met Ser Lys Val Arg Arg Leu His
335 340 345

tat gag ggg cta att ttt agg ttc aag ttc ctc atg ctt atc acc ttg 1467
Tyr Glu Gly Leu Ile Phe Arg Phe Lys Phe Leu Met Leu Ile Thr Leu
350 355 360

gcc tgc gct gcc atg act gtc atc ttc ttc atc gtt agt cag gta acg 1515
Ala Cys Ala Ala Met Thr Val Ile Phe Phe Ile Val Ser Gln Val Thr
365 370 375

gaa ggc cat tgg aaa tgg ggc ggc gtc aca gtc caa gtg aac agt gcc 1563
Glu Gly His Trp Lys Trp Gly Gly Val Thr Val Gln Val Asn Ser Ala
380 385 390 395

ttt ttc aca ggc atc tat ggg atg tgg aat ctg tat gtc ttt gct ctg 1611
Phe Phe Thr Gly Ile Tyr Gly Met Trp Asn Leu Tyr Val Phe Ala Leu

400

405

410

atg ttc ttg tat gca cca tcc cat aaa aac tat gga gaa gac cag tcc 1659
Met Phe Leu Tyr Ala Pro Ser His Lys Asn Tyr Gly Glu Asp Gln Ser
415 420 425

aat gga atg caa ctc cca tgt aaa tcg agg gaa gat tgt gct ttg ttt 1707
Asn Gly Met Gln Leu Pro Cys Lys Ser Arg Glu Asp Cys Ala Leu Phe
430 435 440

gtt tcg gaa ctt tat caa gaa ttg ttc agc gct tcg aaa tat tcc ttc 1755
Val Ser Glu Leu Tyr Gln Glu Leu Phe Ser Ala Ser Lys Tyr Ser Phe
445 450 455

atc aat gac aac gca gct tct ggt att tgagtcaaca aggcaacaca 1802
Ile Asn Asp Asn Ala Ala Ser Gly Ile
460 465

tgtttatcag ctttgcatTT gcagttgtca cagtcacatt gattgtactt gtatacgcac 1862

acaaatacac tcatttagcc tttatctcaa aatgttaaT ataaggaaaa aagcgtcaac 1922

aataaatatt ctttgagtat t 1943

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<211> 460

<212> PRT

<213> Homo sapiens

<400> 147

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20 25 30

Lys Leu Lys Pro Met Thr Ser Cys Phe Leu Phe Thr Phe Pro Ser Pro
35 40 45

Met Asp Val Ser Leu Ala Tyr Arg Asp Asp Ala Phe Ala Glu Trp Thr
50 55 60

Glu Met Ala His Glu Arg Val Pro Arg Lys Leu Lys Cys Thr Phe Thr
65 70 75 80

Ser Pro Lys Thr Pro Glu His Glu Gly Arg Tyr Tyr Glu Cys Asp Val
85 90 95

Leu Pro Phe Met Glu Ile Gly Ser Val Ala His Lys Phe Tyr Leu Leu
100 105 110

Asn Ile Arg Leu Pro Val Asn Glu Lys Lys Lys Ile Asn Val Gly Ile
115 120 125

Gly Glu Ile Lys Asp Ile Arg Leu Val Gly Ile His Gln Asn Gly Gly
130 135 140

tgc ctt ggg gac cca atc att gtg aca aga tcc gag aca ttg aag agg 459

Cys Leu Gly Asp Pro Ile Ile Val Thr Arg Ser Glu Thr Leu Lys Arg

15

20

25

caa ttc caa ggg aaa ttg aag cca atg aca tcg tgt ttt ctg ttc aca 507

Gln Phe Gln Gly Lys Leu Lys Pro Met Thr Ser Cys Phe Leu Phe Thr

30

35

40

ttc ccc tcc ccc atg gac gtt tcc ctg gct tac cgt gat gac gcg ttt 555

Phe Pro Ser Pro Met Asp Val Ser Leu Ala Tyr Arg Asp Asp Ala Phe

45

50

55

60

gct gag tgg act gaa atg gcc cat gaa aga gta cca cgg aaa ctc aaa 603

Ala Glu Trp Thr Glu Met Ala His Glu Arg Val Pro Arg Lys Leu Lys

65

70

75

tgc acc ttc aca tct ccc aag act cca gag cat gag ggc cgt tac tat 651

Cys Thr Phe Thr Ser Pro Lys Thr Pro Glu His Glu Gly Arg Tyr Tyr

80

85

90

gaa tgt gat gtc ctt cct ttc atg gaa att ggg tct gtg gcc cat aag 699

Glu Cys Asp Val Leu Pro Phe Met Glu Ile Gly Ser Val Ala His Lys

95

100

105

ttt tac ctt tta aac atc cgg ctg cct gtg aat gag aag aag aaa atc 747

Phe Tyr Leu Leu Asn Ile Arg Leu Pro Val Asn Glu Lys Lys Lys Ile

110

115

120

aat gtg gga att ggg gag ata aag gat atc cgg ttg gtg ggg atc cac 795

Asn Val Gly Ile Gly Glu Ile Lys Asp Ile Arg Leu Val Gly Ile His

125 130 135 140

caa aat gga ggc ttc acc aag gtg tgg ttt gcc atg aag acc ttc ctt 843

Gln Asn Gly Gly Phe Thr Lys Val Trp Phe Ala Met Lys Thr Phe Leu

145 150 155

acg ccc agc atc ttc atc att atg gtg tgg tat tgg agg agg atc acc 891

Thr Pro Ser Ile Phe Ile Ile Met Val Trp Tyr Trp Arg Arg Ile Thr

160 165 170

atg atg tcc cga ccc cca gtg ctt ctg gaa aaa gtc atc ttt gcc ctt 939

Met Met Ser Arg Pro Pro Val Leu Leu Glu Lys Val Ile Phe Ala Leu

175 180 185

ggg att tcc atg acc ttt atc aat atc cca gtg gaa tgg ttt tcc atc 987

Gly Ile Ser Met Thr Phe Ile Asn Ile Pro Val Glu Trp Phe Ser Ile

190 195 200

ggg ttt gac tgg acc tgg atg ctg ctg ttt ggt gac atc cga cag ggc 1035

Gly Phe Asp Trp Thr Trp Met Leu Leu Phe Gly Asp Ile Arg Gln Gly

205 210 215 220

atc ttc tat gcg atg ctt ctg tcc ttc tgg atc atc ttc tgt ggc gag 1083

Ile Phe Tyr Ala Met Leu Leu Ser Phe Trp Ile Ile Phe Cys Gly Glu

225 230 235

cac atg atg gat cag cac gag cgg aac cac atc gca ggg tat tgg aag 1131

His Met Met Asp Gln His Glu Arg Asn His Ile Ala Gly Tyr Trp Lys

240

245

250

caa gtc gga ccc att gcc gtt ggc tcc ttc tgc ctc ttc ata ttt gac 1179

Gln Val Gly Pro Ile Ala Val Gly Ser Phe Cys Leu Phe Ile Phe Asp

255

260

265

atg tgt gag aga ggg gta caa ctc acg aat ccc ttc tac agt atc tgg 1227

Met Cys Glu Arg Gly Val Gln Leu Thr Asn Pro Phe Tyr Ser Ile Trp

270

275

280

act aca gac att gga aca gag ctg gcc atg gcc ttc atc atc gtg gct 1275

Thr Thr Asp Ile Gly Thr Glu Leu Ala Met Ala Phe Ile Ile Val Ala

285

290

295

300

gga atc tgc ctc tgc ctc tac ttc ctg ttt cta tgc ttc atg gta ttt 1323

Gly Ile Cys Leu Cys Leu Tyr Phe Leu Phe Leu Cys Phe Met Val Phe

305

310

315

cag gtg ttt cgg aac atc agt ggg aag cag tcc agc ctg cca gct atg 1371

Gln Val Phe Arg Asn Ile Ser Gly Lys Gln Ser Ser Leu Pro Ala Met

320

325

330

agc aaa gtc cgg cgg cta cac tat gag ggg cta att ttt agg ttc aag 1419

Ser Lys Val Arg Arg Leu His Tyr Glu Gly Leu Ile Phe Arg Phe Lys

335

340

345

ttc ctc atg ctt atc acc ttg gcc tgc gct gcc atg act gtc atc ttc 1467

Phe Leu Met Leu Ile Thr Leu Ala Cys Ala Ala Met Thr Val Ile Phe

350

355

360

ttc atc gtt agt cag gta acg gaa ggc cat tgg aaa tgg ggc ggc atc 1515
Phe Ile Val Ser Gln Val Thr Glu Gly His Trp Lys Trp Gly Gly Ile
365 370 375 380

aca gtc caa gtg aac agt gcc ttt ttc aca ggc atc tat ggg atg tgg 1563
Thr Val Gln Val Asn Ser Ala Phe Phe Thr Gly Ile Tyr Gly Met Trp
385 390 395

aat ctg tat gtc ttt gct ctg atg ttc ttg tat gca cca tcc cat aaa 1611
Asn Leu Tyr Val Phe Ala Leu Met Phe Leu Tyr Ala Pro Ser His Lys
400 405 410

aac tat gga gaa gac cag tcc aat gga atg caa ctc cca tgt aaa tcg 1659
Asn Tyr Gly Glu Asp Gln Ser Asn Gly Met Gln Leu Pro Cys Lys Ser
415 420 425

agg gaa gat tgt gct ttg ttt gtt tcg gaa ctt tat caa gaa ttg ttc 1707
Arg Glu Asp Cys Ala Leu Phe Val Ser Glu Leu Tyr Gln Glu Leu Phe
430 435 440

agc gct tcg aaa tat tcc ttc atc aat gac aac gca gct tct ggt att 1755
Ser Ala Ser Lys Tyr Ser Phe Ile Asn Asp Asn Ala Ala Ser Gly Ile
445 450 455 460

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542/735

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Cys Pro Pro Tyr Arg Asn Ile Ser Gly His Ile Tyr Asn Gln Asn Val

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Ser Gln Lys Asp Cys Asn Cys Leu His Val Val Glu Pro Met Pro Val

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Gln Gln Arg Trp Lys Leu Gln Val Gln Glu Gln Arg Lys Thr Val Phe

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Asp Arg His Lys Met Leu Ser

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aggctgtcgg ttcggaacat gtctccaccc accccaccct ctgtggctcc aggtttcatt 180

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Ile Leu Gly Ala Leu Glu Arg Asp Arg Leu Thr His Leu Lys His Lys

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Leu Gly Ser Leu Cys Ser Gly Ser Gln Glu Ser Lys Leu Leu His Ala

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Met Val Leu Leu Ala Leu Gly Gln Asp Thr Glu Ala Arg Val Ser Leu

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Glu Ser Leu Lys Met Asn Thr Val Ala Gln Leu Val Ala His Gln Trp

65 70 75

gca gac atg gag acc aca gag ggc cct gag gag cct cca gac ttg tcc 470

Ala Asp Met Glu Thr Thr Glu Gly Pro Glu Glu Pro Pro Asp Leu Ser

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Trp Thr Val Ala Arg Leu Tyr His Leu Leu Ala Glu Glu Asn Leu Cys

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105

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Pro Ala Ser Thr Arg Asp Met Ala Tyr Gln Val Ala Leu Arg Asp Phe

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Ala Ser Gln Gly Asp His Gln Leu Gly Gln Leu Gln Asn Glu Ala Trp

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gtg acc aga agc cag cct cgt ccc att gac aca cca gac tgg agt tgg 758

Val Thr Arg Ser Gln Pro Arg Pro Ile Asp Thr Pro Asp Trp Ser Trp

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gga cat acg tta cac tcc acc aac agc act gcc tca ctg gcc agc cac 806

Gly His Thr Leu His Ser Thr Asn Ser Thr Ala Ser Leu Ala Ser His

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Gly Thr His Gly Pro Ser Lys Leu Cys Asn Thr Pro Leu Asp Thr Gln

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Trp Pro Pro Ser Val Glu Thr Ser Val Ser Leu Gly Leu Pro His Glu

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Asp Ala Leu Ala Ala Pro Asp Thr Ser Val His Cys Pro Ile Glu Cys

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Thr Glu Leu Ser Thr Asn Ser Arg Ser Pro Leu Thr Ser Thr Thr Glu

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Pro Val Gly Asp Asp Ser Leu Gln Asn Thr Thr Ser Ser Ser Pro Pro

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gcc cag cca cca tcc ctc caa gcc tcc cct aag ctg cct cct tcc cct 1286

Ala Gln Pro Pro Ser Leu Gln Ala Ser Pro Lys Leu Pro Pro Ser Pro

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Leu Ser Ser Ala Ser Ser Pro Ser Ser Tyr Pro Ala Pro Pro Thr Ser

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Thr Ser Pro Val Leu Asp His Ser Glu Thr Ser Asp Gln Lys Phe Tyr

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aac ttt gtg gtt atc cat gcc agg gct gat gaa cag gtg gcc cta cgt 1430

Asn Phe Val Val Ile His Ala Arg Ala Asp Glu Gln Val Ala Leu Arg

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| Cys Glu Glu Phe Gln Val Pro Gly Arg Gly Glu Leu His Cys Leu Gln | | | |
| 430 | 435 | 440 | 445 |
| gat gcc atc gat cac tcg ggg ttc acg atc ctg ctc ctg act gct agc | 1574 | | |
| Asp Ala Ile Asp His Ser Gly Phe Thr Ile Leu Leu Leu Thr Ala Ser | | | |
| 450 | 455 | 460 | |
| ttt gat tgc agc ctg agc ctg cat caa atc aac cat gct ctc atg aac | 1622 | | |
| Phe Asp Cys Ser Leu Ser Leu His Gln Ile Asn His Ala Leu Met Asn | | | |
| 465 | 470 | 475 | |
| agc ctt aca cag tct ggg agg cag gac tgt gtg atc ccc ctc ctc cca | 1670 | | |
| Ser Leu Thr Gln Ser Gly Arg Gln Asp Cys Val Ile Pro Leu Leu Pro | | | |
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| ctt gag tgt tcc cag gcc cag ctc agc cca gat aca acc aga ctg ctc | 1718 | | |
| Leu Glu Cys Ser Gln Ala Gln Leu Ser Pro Asp Thr Thr Arg Leu Leu | | | |
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| cac agc att gtg tgg ctg gat gaa cac tcc cca atc ttc gcc aga aag | 1766 | | |
| His Ser Ile Val Trp Leu Asp Glu His Ser Pro Ile Phe Ala Arg Lys | | | |
| 510 | 515 | 520 | 525 |
| gtg gca aac acc ttc aag aca cag aag ctc cag gca cag cgg gta cgc | 1814 | | |
| Val Ala Asn Thr Phe Lys Thr Gln Lys Leu Gln Ala Gln Arg Val Arg | | | |
| 530 | 535 | 540 | |
| 551/735 | | | |

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Trp Lys Lys Ala Gln Glu Ala Arg Thr Leu Lys Glu Gln Ser Ile Gln

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Cys Phe Pro Gln Pro Pro Ser Phe Pro Gln Pro Pro Ser Phe Pro Leu

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35 40 45

Leu Ala Leu Gly Gln Asp Thr Glu Ala Arg Val Ser Leu Glu Ser Leu

50 55 60

Lys Met Asn Thr Val Ala Gln Leu Val Ala His Gln Trp Ala Asp Met

65 70 75 80

all data are from the same source

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90

95

Ala Arg Leu Tyr His Leu Leu Ala Glu Glu Asn Leu Cys Pro Ala Ser

100

105

110

Thr Arg Asp Met Ala Tyr Gln Val Ala Leu Arg Asp Phe Ala Ser Gln

115

120

125

Gly Asp His Gln Leu Gly Gln Leu Gln Asn Glu Ala Trp Asp Arg Cys

130

135

140

Ser Ser Asp Ile Lys Gly Asp Pro Ser Gly Phe Gln Pro Leu His Ser

145

150

155

160

His Gln Gly Ser Leu Gln Pro Pro Ser Ala Ser Pro Ala Val Thr Arg

165

170

175

Ser Gln Pro Arg Pro Ile Asp Thr Pro Asp Trp Ser Trp Gly His Thr

180

185

190

Leu His Ser Thr Asn Ser Thr Ala Ser Leu Ala Ser His Leu Glu Ile

195

200

205

Ser Gln Ser Pro Thr Leu Ala Phe Leu Ser Ser His His Gly Thr His

210

215

220

Gly Pro Ser Lys Leu Cys Asn Thr Pro Leu Asp Thr Gln Glu Pro Gln

225

230

235

240

385 390 395 400

Val Ile His Ala Arg Ala Asp Glu Gln Val Ala Leu Arg Ile Arg Glu

405 410 415

Lys Leu Glu Thr Leu Gly Val Pro Asp Gly Ala Thr Phe Cys Glu Glu

420 425 430

Phe Gln Val Pro Gly Arg Gly Glu Leu His Cys Leu Gln Asp Ala Ile

435 440 445

Asp His Ser Gly Phe Thr Ile Leu Leu Leu Thr Ala Ser Phe Asp Cys

450 455 460

Ser Leu Ser Leu His Gln Ile Asn His Ala Leu Met Asn Ser Leu Thr

465 470 475 480

Gln Ser Gly Arg Gln Asp Cys Val Ile Pro Leu Leu Pro Leu Glu Cys

485 490 495

Ser Gln Ala Gln Leu Ser Pro Asp Thr Thr Arg Leu Leu His Ser Ile

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Val Trp Leu Asp Glu His Ser Pro Ile Phe Ala Arg Lys Val Ala Asn

515 520 525

Thr Phe Lys Thr Gln Lys Leu Gln Ala Gln Arg Val Arg Trp Lys Lys

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Ala Gln Glu Ala Arg Thr Leu Lys Glu Gln Ser Ile Gln Leu Glu Ala
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Glu Arg Gln Asn Val Ala Ala Ile Ser Ala Ala Tyr Thr Ala Tyr Val
565 570 575

His Ser Tyr Arg Ala Trp Gln Ala Glu Met Asn Lys Leu Gly Val Ala
580 585 590

Phe Gly Lys Asn Leu Ser Leu Gly Thr Pro Thr Pro Ser Trp Pro Gly
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Cys Pro Gln Pro Ile Pro Ser His Pro Gln Gly Gly Thr Pro Val Phe
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Pro Tyr Ser Pro Gln Pro Pro Ser Phe Pro Gln Pro Pro Cys Phe Pro
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Gln Pro Pro Ser Phe Pro Gln Pro Pro Ser Phe Pro Leu Pro Pro Val
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Ser Ser Pro Gln Ser Gln Ser Phe Pro Ser Ala Ser Ser Pro Ala Pro
660 665 670

Gln Thr Pro Gly Pro Gln Pro Leu Ile Ile His His Ala Gln Met Val
675 680 685

Gln Leu Gly Val Asn Asn His Met Trp Gly His Thr Gly Ala Gln Ser
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$\langle 221 \rangle$ CDS

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Met Ala Cys Thr Gly Pro

1

5

tca ctt cct agc gcc ttc gac att cta ggt gca gca ggc cag gac aag 162

Ser Leu Pro Ser Ala Phe Asp Ile Leu Gly Ala Ala Gly Gln Asp Lys

10

15

20

ctc ttg tat ctg aag cac aaa ctg aag acc cca cgc cca ggc tgc cag 210

Leu Leu Tyr Leu Lys His Lys Leu Lys Thr Pro Arg Pro Gly Cys Gln

25

30

35

ggg cag gac ctc ctg cat gcc atg gtt ctc ctg aag ctg ggc cag gaa 258

Gly Gln Asp Leu Leu His Ala Met Val Leu Leu Lys Leu Gly Gln Glu

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45

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act gag gcc agg atc tct cta gag gca ttg aag gcc gat gcg gtg gcc 306

Thr Glu Ala Arg Ile Ser Leu Glu Ala Leu Lys Ala Asp Ala Val Ala

55

60

65

70

cgg ctg gtg gcc cgc cag tgg gct ggc gtg gac agc acc gag gac cca 354

Arg Leu Val Ala Arg Gln Trp Ala Gly Val Asp Ser Thr Glu Asp Pro

75

80

85

gag gag ccc cca gat gtg tcc tgg gct gtg gcc cgc ttg tac cac ctg 402

Glu Glu Pro Pro Asp Val Ser Trp Ala Val Ala Arg Leu Tyr His Leu

90

95

100

ctg gct gag gag aag ctg tgc ccc gcc tcg ctg cgg gac gtg gcc tac 450

Leu Ala Glu Glu Lys Leu Cys Pro Ala Ser Leu Arg Asp Val Ala Tyr

105

110

115

cag gaa gcc gtc cgc acc ctc agc tcc agg gac gac cac cgg ctg ggg 498

Gln Glu Ala Val Arg Thr Leu Ser Ser Arg Asp Asp His Arg Leu Gly

120

125

130

gaa ctt cag gat gag gcc cga aac cgg tgt ggg tgg gac att gct ggg 546

Glu Leu Gln Asp Glu Ala Arg Asn Arg Cys Gly Trp Asp Ile Ala Gly
 135 140 145 150

gat cca ggg agc atc cgg acg ctc cag tcc aat ctg ggc tgc ctc cca 594
 Asp Pro Gly Ser Ile Arg Thr Leu Gln Ser Asn Leu Gly Cys Leu Pro
 155 160 165

cca tcc tcg gct ttg ccc tct ggg acc agg agc ctc cca cgc ccc att 642
 Pro Ser Ser Ala Leu Pro Ser Gly Thr Arg Ser Leu Pro Arg Pro Ile
 170 175 180

gac ggt gtt tcg gac tgg agc caa ggg tgc tcc ctg cga tcc act ggc 690
 Asp Gly Val Ser Asp Trp Ser Gln Gly Cys Ser Leu Arg Ser Thr Gly
 185 190 195

agc cct gcc tcc ctg gcc agc aac ttg gaa atc agc cag tcc cct acc 738
 Ser Pro Ala Ser Leu Ala Ser Asn Leu Glu Ile Ser Gln Ser Pro Thr
 200 205 210

atg ccc ttc ctc agc ctg cac cgc agc cca cat ggg ccc agc aag ctc 786
 Met Pro Phe Leu Ser Leu His Arg Ser Pro His Gly Pro Ser Lys Leu
 215 220 225 230

tgt gac gac ccc cag gcc agc ttg gtg ccc gag cct gtc ccc ggt ggc 834
 Cys Asp Asp Pro Gln Ala Ser Leu Val Pro Glu Pro Val Pro Gly Gly
 235 240 245

tgc cag gag cct gag gag atg agc tgg ccg cca tcg ggg gag att gcc 882
 Cys Gln Glu Pro Glu Glu Met Ser Trp Pro Pro Ser Gly Glu Ile Ala
 561/735

250

255

260

agc cca cca gag ctg cca agc agc cca cct cct ggg ctt ccc gaa gtg 930

Ser Pro Pro Glu Leu Pro Ser Ser Pro Pro Pro Gly Leu Pro Glu Val

265

270

275

gcc cca gat gca acc tcc act ggc ctc cct gat acc ccc gca gct cca 978

Ala Pro Asp Ala Thr Ser Thr Gly Leu Pro Asp Thr Pro Ala Ala Pro

280

285

290

gaa acc agc acc aac tac cca gtg gag tgc acc gag ggg tct gca ggc 1026

Glu Thr Ser Thr Asn Tyr Pro Val Glu Cys Thr Glu Gly Ser Ala Gly

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ccc cag tct ctc ccc ttg cct att ctg gag ccg gtc aaa aac ccc tgc 1074

Pro Gln Ser Leu Pro Leu Pro Ile Leu Glu Pro Val Lys Asn Pro Cys

315

320

325

tct gtc aaa gac cag acg cca ctc caa ctt tct gta gaa gat acc acc 1122

Ser Val Lys Asp Gln Thr Pro Leu Gln Leu Ser Val Glu Asp Thr Thr

330

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340

tct cca aat acc aag ccg tgc cca cct act ccc acc acc cca gaa aca 1170

Ser Pro Asn Thr Lys Pro Cys Pro Pro Thr Pro Thr Thr Pro Glu Thr

345

350

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tcc cct cct cct cct cct cct cct cct tca tct act cct tgt tca gct 1218

Ser Pro Pro Pro Pro Pro Pro Pro Pro Ser Ser Thr Pro Cys Ser Ala

360

365

370

cac ctg acc ccc tcc tcc ctg ttc cct tcc tcc ctg gaa tca tca tcg 1266

His Leu Thr Pro Ser Ser Leu Phe Pro Ser Ser Leu Glu Ser Ser Ser

375 380 385 390

gaa cag aaa ttc tat aac ttt gtg atc ctc cac gcc agg gca gac gaa 1314

Glu Gln Lys Phe Tyr Asn Phe Val Ile Leu His Ala Arg Ala Asp Glu

395 400 405

cac atc gcc ctg cgg gtt cgg gag aag ctg gag gcc ctt ggc gtg ccc 1362

His Ile Ala Leu Arg Val Arg Glu Lys Leu Glu Ala Leu Gly Val Pro

410 415 420

gac ggg gcc acc ttc tgc gag gat ttc cag gtg ccg ggg cgc ggg gag 1410

Asp Gly Ala Thr Phe Cys Glu Asp Phe Gln Val Pro Gly Arg Gly Glu

425 430 435

ctg agc tgc ctg cag gac gcc ata gac cac tca gct ttc atc atc cta 1458

Leu Ser Cys Leu Gln Asp Ala Ile Asp His Ser Ala Phe Ile Ile Leu

440 445 450

ctt ctc acc tcc aac ttc gac tgt cgc ctg agc ctg cac cag gtg aac 1506

Leu Leu Thr Ser Asn Phe Asp Cys Arg Leu Ser Leu His Gln Val Asn

455 460 465 470

caa gcc atg atg agc aac ctc acg cga cag ggg tcg cca gac tgt gtc 1554

Gln Ala Met Met Ser Asn Leu Thr Arg Gln Gly Ser Pro Asp Cys Val

475 480 485

atc ccc ttc ctg ccc ctg gag agc tcc ccg gcc cag ctc agc tcc gac 1602
 Ile Pro Phe Leu Pro Leu Glu Ser Ser Pro Ala Gln Leu Ser Ser Asp
 490 495 500

acg gcc agc ctg ctc tcc ggg ctg gtg cgg ctg gac gaa cac tcc cag 1650
 Thr Ala Ser Leu Leu Ser Gly Leu Val Arg Leu Asp Glu His Ser Gln
 505 510 515

atc ttc gcc agg aag gtg gcc aac acc ttc aag ccc cac agg ctt cag 1698
 Ile Phe Ala Arg Lys Val Ala Asn Thr Phe Lys Pro His Arg Leu Gln
 520 525 530

gcc cga aag gcc atg tgg agg aag gaa cag gac acc cga gcc ctg cgg 1746
 Ala Arg Lys Ala Met Trp Arg Lys Glu Gln Asp Thr Arg Ala Leu Arg
 535 540 545 550

gaa cag agc caa cac ctg gac ggt gag cgg atg cag gcg gcg gca ctg 1794
 Glu Gln Ser Gln His Leu Asp Gly Glu Arg Met Gln Ala Ala Ala Leu
 555 560 565

aac gca gcc tac tca gcc tac ctc cag agc tac ttg tcc tac cag gca 1842
 Asn Ala Ala Tyr Ser Ala Tyr Leu Gln Ser Tyr Leu Ser Tyr Gln Ala
 570 575 580

cag atg gag cag ctc cag gtg gct ttt ggg agc cac atg tca ttt ggg 1890
 Gln Met Glu Gln Leu Gln Val Ala Phe Gly Ser His Met Ser Phe Gly
 585 590 595

act ggg gcg ccc tat ggg gct cga atg ccc ttt ggg ggc cag gtg ccc 1938
 564/735

Thr Gly Ala Pro Tyr Gly Ala Arg Met Pro Phe Gly Gly Gln Val Pro

600

605

610

ctg gga gcc ccg cca ccc ttt ccc act tgg ccg ggg tgc ccg cag ccg 1986

Leu Gly Ala Pro Pro Pro Phe Pro Thr Trp Pro Gly Cys Pro Gln Pro

615

620

625

630

cca ccc ctg cac gca tgg cag gct ggc acc ccc cca ccg ccc tcc cca 2034

Pro Pro Leu His Ala Trp Gln Ala Gly Thr Pro Pro Pro Pro Ser Pro

635

640

645

cag cca gca gcc ttt cca cag tca ctg ccc ttc ccg cag tcc cca gcc 2082

Gln Pro Ala Ala Phe Pro Gln Ser Leu Pro Phe Pro Gln Ser Pro Ala

650

655

660

ttc cct acg gcc tca ccc gca ccc cct cag agc cca ggg ctg caa ccc 2130

Phe Pro Thr Ala Ser Pro Ala Pro Pro Gln Ser Pro Gly Leu Gln Pro

665

670

675

ctc att atc cac cac gca cag atg gta cag ctg ggg ctg aac aac cac 2178

Leu Ile Ile His His Ala Gln Met Val Gln Leu Gly Leu Asn Asn His

680

685

690

atg tgg aac cag aga ggg tcc cag gcg ccc gag gac aag acg cag gag 2226

Met Trp Asn Gln Arg Gly Ser Gln Ala Pro Glu Asp Lys Thr Gln Glu

695

700

705

710

gca gaa tgaccgcgtg tcttgccctg accacctggg gaacaccctt ggaccaggc 2282

Ala Glu

atcggccagg accccataga gcaccccggt ctgccctgtg ccctgtggac agtggaagat 2342

gaggtcacatc gccactttca ggacattgtc cgggagccct tcatttagga caaaacgggc 2402

gcgatgatgc cctggctttc aggggtggta gaactggata cggtgtttac aattccaatc 2462

tctctatttc tgggtgaagg gtcttggtgg tgggggtatt gctacggtct ttttaattata 2522

ataaatatattt attgaatgct tc 2544

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<212> PRT

<213> Homo sapiens

<400> 154

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Ala Ala Gly Gln Asp Lys Leu Leu Tyr Leu Lys His Lys Leu Lys Thr

20 25 30

Pro Arg Pro Gly Cys Gln Gly Gln Asp Leu Leu His Ala Met Val Leu

35 40 45

Leu Lys Leu Gly Gln Glu Thr Glu Ala Arg Ile Ser Leu Glu Ala Leu

50 55 60

Lys Ala Asp Ala Val Ala Arg Leu Val Ala Arg Gln Trp Ala Gly Val
65 70 75 80

Asp Ser Thr Glu Asp Pro Glu Glu Pro Pro Asp Val Ser Trp Ala Val
85 90 95

Ala Arg Leu Tyr His Leu Leu Ala Glu Glu Lys Leu Cys Pro Ala Ser
100 105 110

Leu Arg Asp Val Ala Tyr Gln Glu Ala Val Arg Thr Leu Ser Ser Arg
115 120 125

Asp Asp His Arg Leu Gly Glu Leu Gln Asp Glu Ala Arg Asn Arg Cys
130 135 140

Gly Trp Asp Ile Ala Gly Asp Pro Gly Ser Ile Arg Thr Leu Gln Ser
145 150 155 160

Asn Leu Gly Cys Leu Pro Pro Ser Ser Ala Leu Pro Ser Gly Thr Arg
165 170 175

Ser Leu Pro Arg Pro Ile Asp Gly Val Ser Asp Trp Ser Gln Gly Cys
180 185 190

Ser Leu Arg Ser Thr Gly Ser Pro Ala Ser Leu Ala Ser Asn Leu Glu
195 200 205

Ile Ser Gln Ser Pro Thr Met Pro Phe Leu Ser Leu His Arg Ser Pro
567/735

| | | | |
|-----------------------------------------------------------------|-----|-----|-----|
| 210 | 215 | 220 | |
| His Gly Pro Ser Lys Leu Cys Asp Asp Pro Gln Ala Ser Leu Val Pro | | | |
| 225 | 230 | 235 | 240 |
| Glu Pro Val Pro Gly Gly Cys Gln Glu Pro Glu Glu Met Ser Trp Pro | | | |
| 245 | 250 | 255 | |
| Pro Ser Gly Glu Ile Ala Ser Pro Pro Glu Leu Pro Ser Ser Pro Pro | | | |
| 260 | 265 | 270 | |
| Pro Gly Leu Pro Glu Val Ala Pro Asp Ala Thr Ser Thr Gly Leu Pro | | | |
| 275 | 280 | 285 | |
| Asp Thr Pro Ala Ala Pro Glu Thr Ser Thr Asn Tyr Pro Val Glu Cys | | | |
| 290 | 295 | 300 | |
| Thr Glu Gly Ser Ala Gly Pro Gln Ser Leu Pro Leu Pro Ile Leu Glu | | | |
| 305 | 310 | 315 | 320 |
| Pro Val Lys Asn Pro Cys Ser Val Lys Asp Gln Thr Pro Leu Gln Leu | | | |
| 325 | 330 | 335 | |
| Ser Val Glu Asp Thr Thr Ser Pro Asn Thr Lys Pro Cys Pro Pro Thr | | | |
| 340 | 345 | 350 | |
| Pro Thr Thr Pro Glu Thr Ser Pro Pro Pro Pro Pro Pro Pro Ser | | | |
| 355 | 360 | 365 | |

Ser Thr Pro Cys Ser Ala His Leu Thr Pro Ser Ser Leu Phe Pro Ser
370 375 380

Ser Leu Glu Ser Ser Ser Glu Gln Lys Phe Tyr Asn Phe Val Ile Leu
385 390 395 400

His Ala Arg Ala Asp Glu His Ile Ala Leu Arg Val Arg Glu Lys Leu
405 410 415

Glu Ala Leu Gly Val Pro Asp Gly Ala Thr Phe Cys Glu Asp Phe Gln
420 425 430

Val Pro Gly Arg Gly Glu Leu Ser Cys Leu Gln Asp Ala Ile Asp His
435 440 445

Ser Ala Phe Ile Ile Leu Leu Leu Thr Ser Asn Phe Asp Cys Arg Leu
450 455 460

Ser Leu His Gln Val Asn Gln Ala Met Met Ser Asn Leu Thr Arg Gln
465 470 475 480

Gly Ser Pro Asp Cys Val Ile Pro Phe Leu Pro Leu Glu Ser Ser Pro
485 490 495

Ala Gln Leu Ser Ser Asp Thr Ala Ser Leu Leu Ser Gly Leu Val Arg
500 505 510

Leu Asp Glu His Ser Gln Ile Phe Ala Arg Lys Val Ala Asn Thr Phe
515 520 525

Lys Pro His Arg Leu Gln Ala Arg Lys Ala Met Trp Arg Lys Glu Gln
530 535 540

Asp Thr Arg Ala Leu Arg Glu Gln Ser Gln His Leu Asp Gly Glu Arg
545 550 555 560

Met Gln Ala Ala Ala Leu Asn Ala Ala Tyr Ser Ala Tyr Leu Gln Ser
565 570 575

Tyr Leu Ser Tyr Gln Ala Gln Met Glu Gln Leu Gln Val Ala Phe Gly
580 585 590

Ser His Met Ser Phe Gly Thr Gly Ala Pro Tyr Gly Ala Arg Met Pro
595 600 605

Phe Gly Gly Gln Val Pro Leu Gly Ala Pro Pro Pro Phe Pro Thr Trp
610 615 620

Pro Gly Cys Pro Gln Pro Pro Pro Leu His Ala Trp Gln Ala Gly Thr
625 630 635 640

Pro Pro Pro Pro Ser Pro Gln Pro Ala Ala Phe Pro Gln Ser Leu Pro
645 650 655

Phe Pro Gln Ser Pro Ala Phe Pro Thr Ala Ser Pro Ala Pro Pro Gln
660 665 670

Ser Pro Gly Leu Gln Pro Leu Ile Ile His His Ala Gln Met Val Gln
570/735

675

680

685

Leu Gly Leu Asn Asn His Met Trp Asn Gln Arg Gly Ser Gln Ala Pro

690

695

700

Glu Asp Lys Thr Gln Glu Ala Glu

705

710

<210> 155

<211> 3456

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (281).. (3016)

<400> 155

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ggaggagagc tctgtggatg gcaaagggga ccggaagagc acaggcctga aactctccaa 180

gaagaaagca aggaggagac acacggatga cccaagcaag gaatgcttca ctctgaaatt 240

tgacctgaat gtggacattg agacagagat cgtcccagcc atg aag aag aag tca 295

Met Lys Lys Lys Ser

1

5

ctg ggg gag gtg ctg ctg cct gta ttt gaa agg aag ggc att gcg ctg 343
Leu Gly Glu Val Leu Leu Pro Val Phe Glu Arg Lys Gly Ile Ala Leu
10 15 20

ggc aaa gtg gac atc tac ctg gac cag tcc aac aca ccc ctg tcc ctc 391
Gly Lys Val Asp Ile Tyr Leu Asp Gln Ser Asn Thr Pro Leu Ser Leu
25 30 35

acc ttc gag gcc tac agg ttc ggg gga cac tac ctt cgt gtc aaa gcc 439
Thr Phe Glu Ala Tyr Arg Phe Gly Gly His Tyr Leu Arg Val Lys Ala
40 45 50

cca gcc aag cct gga gat gag ggc aag gtg gag cag ggc atg aag gac 487
Pro Ala Lys Pro Gly Asp Glu Gly Lys Val Glu Gln Gly Met Lys Asp
55 60 65

tcc aag tcc ctg agt ttg ccg att ctg cgg cca gct ggg acc ggg ccc 535
Ser Lys Ser Leu Ser Leu Pro Ile Leu Arg Pro Ala Gly Thr Gly Pro
70 75 80 85

ccc gcc ctg gag cgt gtg gac gcc cag agc cgc cgg gag agc ctg gac 583
Pro Ala Leu Glu Arg Val Asp Ala Gln Ser Arg Arg Glu Ser Leu Asp
90 95 100

atc ttg gcc cct ggc cgc cgc cgc aag aac atg tcg gag ttc ctg ggg 631
Ile Leu Ala Pro Gly Arg Arg Arg Lys Asn Met Ser Glu Phe Leu Gly
572/735

105

110

115

gag gcg agc atc ccc ggg cag gag ccc ccc acg ccc tcc agc tgc tct 679

Glu Ala Ser Ile Pro Gly Gln Glu Pro Pro Thr Pro Ser Ser Cys Ser

120

125

130

ctg ccc agc ggc agc agt ggc agc acc aac act ggc gac agc tgg aag 727

Leu Pro Ser Gly Ser Ser Gly Ser Thr Asn Thr Gly Asp Ser Trp Lys

135

140

145

aac cgg gcg gcc agt cgc ttc agc ggc ttt ttc agc tcc ggc ccc agc 775

Asn Arg Ala Ala Ser Arg Phe Ser Gly Phe Phe Ser Ser Gly Pro Ser

150

155

160

165

acc agc gcc ttt ggc cgg gag gta gac aag atg gag cag ctg gag ggc 823

Thr Ser Ala Phe Gly Arg Glu Val Asp Lys Met Glu Gln Leu Glu Gly

170

175

180

aag ctg cac acc tac agc ctc ttc ggg ctg ccc agg ctg ccc cgg ggc 871

Lys Leu His Thr Tyr Ser Leu Phe Gly Leu Pro Arg Leu Pro Arg Gly

185

190

195

ctg cgc ttc gac cat gac tcc tgg gag gag gag tac gat gaa gac gag 919

Leu Arg Phe Asp His Asp Ser Trp Glu Glu Glu Tyr Asp Glu Asp Glu

200

205

210

gat gag gac aat gcc tgc ctg agg ctg gag gac agc tgg cgg gag ctc 967

Asp Glu Asp Asn Ala Cys Leu Arg Leu Glu Asp Ser Trp Arg Glu Leu

215

220

225

atc cgc tac tgc atg gag gag gag ggc tgc atg gag tac atg cgc ggc 1351

Ile Arg Tyr Cys Met Glu Glu Glu Gly Cys Met Glu Tyr Met Arg Gly

345

350

355

ctg ctg cgc gac aac gac ctc ttc cgg gcc tac atc acg tgg gcg gag 1399

Leu Leu Arg Asp Asn Asp Leu Phe Arg Ala Tyr Ile Thr Trp Ala Glu

360

365

370

aag cac cca cag tgc cag agg ctg aag ctg agc gac atg ctg gcc aaa 1447

Lys His Pro Gln Cys Gln Arg Leu Lys Leu Ser Asp Met Leu Ala Lys

375

380

385

ccc cac cag cgg ctc acc aag tac ccg ctg ctg ctc aag tcg gtg ctg 1495

Pro His Gln Arg Leu Thr Lys Tyr Pro Leu Leu Leu Lys Ser Val Leu

390

395

400

405

agg aag acc gag gag ccg cgc gcc aag gag gcc gtc gtc gcc atg atc 1543

Arg Lys Thr Glu Glu Pro Arg Ala Lys Glu Ala Val Val Ala Met Ile

410

415

420

ggc tcc gtg gag cgc ttc atc cac cac gtg aac gcg tgc atg cgg cag 1591

Gly Ser Val Glu Arg Phe Ile His His Val Asn Ala Cys Met Arg Gln

425

430

435

cgg cag gag cgg cag cgg ctg gcg gcc gtg gtg agc cgc atc gac gcc 1639

Arg Gln Glu Arg Gln Arg Leu Ala Ala Val Val Ser Arg Ile Asp Ala

440

445

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tac gag gtg gtg gaa agc agc agc gac gaa gtg gac aag ctc ctg aag 1687

Tyr Glu Val Val Glu Ser Ser Ser Asp Glu Val Asp Lys Leu Leu Lys

455

460

465

gaa ttt ctg cac ctg gac ttg aca gcg ccc atc cct ggc gcc tcc ccg 1735

Glu Phe Leu His Leu Asp Leu Thr Ala Pro Ile Pro Gly Ala Ser Pro

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475

480

485

gag gag acg cgg cag ctg ctg ctg gag ggg agc ctg agg atg aag gag 1783

Glu Glu Thr Arg Gln Leu Leu Leu Glu Gly Ser Leu Arg Met Lys Glu

490

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ggg aag gac agc aag atg gat gtg tac tgc ttc ctc ttc acg gat ctg 1831

Gly Lys Asp Ser Lys Met Asp Val Tyr Cys Phe Leu Phe Thr Asp Leu

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ctg ttg gtg acc aaa gca gtg aag aag gca gag agg acc agg gtc atc 1879

Leu Leu Val Thr Lys Ala Val Lys Lys Ala Glu Arg Thr Arg Val Ile

520

525

530

agg cca ccc ctg ctc gtg gac aag att gtg tgc cgg gag cta cgg gac 1927

Arg Pro Pro Leu Leu Val Asp Lys Ile Val Cys Arg Glu Leu Arg Asp

535

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cct ggg tcc ttc ctc ctt atc tac ctg aat gag ttt cac agt gct gta 1975

Pro Gly Ser Phe Leu Leu Ile Tyr Leu Asn Glu Phe His Ser Ala Val

550

555

560

565

ggg gcc tac acg ttc cag gcc agt ggc cag gcc ttg tgc cgt ggc tgg 2023

Gly Ala Tyr Thr Phe Gln Ala Ser Gly Gln Ala Leu Cys Arg Gly Trp

576/735

570

575

580

gtg gac acc att tac aat gcc cag aac cag ctg caa cag ctg cgt gca 2071

Val Asp Thr Ile Tyr Asn Ala Gln Asn Gln Leu Gln Gln Leu Arg Ala

585

590

595

cag gag ccc cca ggc agt cag cag ccc ctg cag agc ctg gaa gag gag 2119

Gln Glu Pro Pro Gly Ser Gln Gln Pro Leu Gln Ser Leu Glu Glu Glu

600

605

610

gag gat gag cag gag gag gaa gag gag gag gag gag gag gag gag gaa 2167

Glu Asp Glu Gln Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu

615

620

625

ggc gag gac agt ggc act tca gct gcc agc tcc cct acc atc atg cgg 2215

Gly Glu Asp Ser Gly Thr Ser Ala Ala Ser Ser Pro Thr Ile Met Arg

630

635

640

645

aaa agc agc ggc agc ccc gac tct cag cac tgt gcc tca gat ggc tcc 2263

Lys Ser Ser Gly Ser Pro Asp Ser Gln His Cys Ala Ser Asp Gly Ser

650

655

660

acg gag acc ctg gcc atg gtt gtg gta gag cct ggg gac acg ctg tcc 2311

Thr Glu Thr Leu Ala Met Val Val Val Glu Pro Gly Asp Thr Leu Ser

665

670

675

tcc ccc gag ttc gac agc ggt cct ttc agc tcc cag tct gat gag acc 2359

Ser Pro Glu Phe Asp Ser Gly Pro Phe Ser Ser Gln Ser Asp Glu Thr

680

685

690

tct ctc agc acc act gcc tca tct gcc acg ccc acc agt gag ctg ctg 2407

Ser Leu Ser Thr Thr Ala Ser Ser Ala Thr Pro Thr Ser Glu Leu Leu

695

700

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ccc ctg ggt ccg gtg gac ggc cgc tcc tgc tcc atg gac tct gcc tac 2455

Pro Leu Gly Pro Val Asp Gly Arg Ser Cys Ser Met Asp Ser Ala Tyr

710

715

720

725

ggc acc ctc tcc cca acc tcc tta caa gac ttt gtg gcc cca ggc cca 2503

Gly Thr Leu Ser Pro Thr Ser Leu Gln Asp Phe Val Ala Pro Gly Pro

730

735

740

atg gca gag cta gtg cct cgg gcc cca gag tcc cca cga gtt cct tcc 2551

Met Ala Glu Leu Val Pro Arg Ala Pro Glu Ser Pro Arg Val Pro Ser

745

750

755

cct cca ccc teg ccc cgt ctc cgc cgc cgc acc cct gtc cag ctg ttg 2599

Pro Pro Pro Ser Pro Arg Leu Arg Arg Arg Thr Pro Val Gln Leu Leu

760

765

770

agc tgc ccg ccc cac ctg ctc aag tct aag tcc gag gcc agc ctc ctc 2647

Ser Cys Pro Pro His Leu Leu Lys Ser Lys Ser Glu Ala Ser Leu Leu

775

780

785

cag ctg ctg gca ggg gct ggc acc cat ggg aca ccc tct gcc ccc agc 2695

Gln Leu Leu Ala Gly Ala Gly Thr His Gly Thr Pro Ser Ala Pro Ser

790

795

800

805

cgc agc ctg tca gag ctc tgc ctg gct gtt cca gcc cca ggt att agg 2743

Arg Ser Leu Ser Glu Leu Cys Leu Ala Val Pro Ala Pro Gly Ile Arg

810

815

820

act cag ggc tcc cct cag gaa gct ggg ccc agc tgg gat tgc cga ggg 2791

Thr Gln Gly Ser Pro Gln Glu Ala Gly Pro Ser Trp Asp Cys Arg Gly

825

830

835

gcc cct agc cct ggc agc ggt cct ggg cta gtc ggc tgc ctg gcc ggg 2839

Ala Pro Ser Pro Gly Ser Gly Pro Gly Leu Val Gly Cys Leu Ala Gly

840

845

850

gaa cct gca ggc tcc cac agg aag agg tgt gga gac ctg ccc tcg ggg 2887

Glu Pro Ala Gly Ser His Arg Lys Arg Cys Gly Asp Leu Pro Ser Gly

855

860

865

gcc tct ccc agg gtc cag cct gag ccc cca cca ggg gtc tct gcc cag 2935

Ala Ser Pro Arg Val Gln Pro Glu Pro Pro Pro Gly Val Ser Ala Gln

870

875

880

885

cac agg aag ctg acc ctg gcc cag ctc tac cga atc agg acc acc ctg 2983

His Arg Lys Leu Thr Leu Ala Gln Leu Tyr Arg Ile Arg Thr Thr Leu

890

895

900

ctg ctt aac tcc acg ctc act gcc tcg gag gtc tgagcagagg gaggcccca 3036

Leu Leu Asn Ser Thr Leu Thr Ala Ser Glu Val

905

910

agagtgccat tgaccaagag acagcagaca gcctgcctcc tggggcgtgc cggcacctgc 3096

ttcagctact gcctcctgta tgcattgagcc ggatgctggg caggatccct gcctacgccc 3156

gggcccgatt tgcgctttgc cggactggat ggagtggagg aggcccaggc cacagtagca 3216

ccccacctgc ccaggcagcc cctcgtcacc tactccccga agttaccagc tcagctcgag 3276

tcttcagggc tgggctecta ggctgcccatt cctacttcta ccctcactgg cctccagtgg 3336

gattcactcc tgcctgccc ccacctccc agtcccacag gccacccctg gcttgggctg 3396

ggttctgtga agttacgtat ttattgagct ttgtgttctt ttataaagac ttgtctagac 3456

<210> 156

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<212> PRT

<213> Homo sapiens

<400> 156

Met Lys Lys Lys Ser Leu Gly Glu Val Leu Leu Pro Val Phe Glu Arg

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Lys Gly Ile Ala Leu Gly Lys Val Asp Ile Tyr Leu Asp Gln Ser Asn

20 25 30

Thr Pro Leu Ser Leu Thr Phe Glu Ala Tyr Arg Phe Gly Gly His Tyr

35 40 45

Leu Arg Val Lys Ala Pro Ala Lys Pro Gly Asp Glu Gly Lys Val Glu

50

55

60

Gln Gly Met Lys Asp Ser Lys Ser Leu Ser Leu Pro Ile Leu Arg Pro

65

70

75

80

Ala Gly Thr Gly Pro Pro Ala Leu Glu Arg Val Asp Ala Gln Ser Arg

85

90

95

Arg Glu Ser Leu Asp Ile Leu Ala Pro Gly Arg Arg Arg Lys Asn Met

100

105

110

Ser Glu Phe Leu Gly Glu Ala Ser Ile Pro Gly Gln Glu Pro Pro Thr

115

120

125

Pro Ser Ser Cys Ser Leu Pro Ser Gly Ser Ser Gly Ser Thr Asn Thr

130

135

140

Gly Asp Ser Trp Lys Asn Arg Ala Ala Ser Arg Phe Ser Gly Phe Phe

145

150

155

160

Ser Ser Gly Pro Ser Thr Ser Ala Phe Gly Arg Glu Val Asp Lys Met

165

170

175

Glu Gln Leu Glu Gly Lys Leu His Thr Tyr Ser Leu Phe Gly Leu Pro

180

185

190

Arg Leu Pro Arg Gly Leu Arg Phe Asp His Asp Ser Trp Glu Glu Glu

195

200

205

Tyr Asp Glu Asp Glu Asp Glu Asp Asn Ala Cys Leu Arg Leu Glu Asp

210

215

220

Ser Trp Arg Glu Leu Ile Asp Gly His Glu Lys Leu Thr Arg Arg Gln

225

230

235

240

Cys His Gln Gln Glu Ala Val Trp Glu Leu Leu His Thr Glu Ala Ser

245

250

255

Tyr Ile Arg Lys Leu Arg Val Ile Ile Asn Leu Phe Leu Cys Cys Leu

260

265

270

Leu Asn Leu Gln Glu Ser Gly Leu Leu Cys Glu Val Glu Ala Glu Arg

275

280

285

Leu Phe Ser Asn Ile Pro Glu Ile Ala Gln Leu His Arg Arg Leu Trp

290

295

300

Ala Ser Val Met Ala Pro Val Leu Glu Lys Ala Arg Arg Thr Arg Ala

305

310

315

320

Leu Leu Gln Pro Gly Asp Phe Leu Lys Gly Phe Lys Met Phe Gly Ser

325

330

335

Leu Phe Lys Pro Tyr Ile Arg Tyr Cys Met Glu Glu Glu Gly Cys Met

340

345

350

Glu Tyr Met Arg Gly Leu Leu Arg Asp Asn Asp Leu Phe Arg Ala Tyr



365

380

400

415

430

445

460

480

495

510

Leu Phe Thr Asp Leu Leu Leu Val Thr Lys Ala Val Lys Lys Ala Glu

515

520

525

Arg Thr Arg Val Ile Arg Pro Pro Leu Leu Val Asp Lys Ile Val Cys

530

535

540

Arg Glu Leu Arg Asp Pro Gly Ser Phe Leu Leu Ile Tyr Leu Asn Glu

545

550

555

560

Phe His Ser Ala Val Gly Ala Tyr Thr Phe Gln Ala Ser Gly Gln Ala

565

570

575

Leu Cys Arg Gly Trp Val Asp Thr Ile Tyr Asn Ala Gln Asn Gln Leu

580

585

590

Gln Gln Leu Arg Ala Gln Glu Pro Pro Gly Ser Gln Gln Pro Leu Gln

595

600

605

Ser Leu Glu Glu Glu Glu Asp Glu Gln Glu Glu Glu Glu Glu Glu

610

615

620

Glu Glu Glu Glu Glu Gly Glu Asp Ser Gly Thr Ser Ala Ala Ser Ser

625

630

635

640

Pro Thr Ile Met Arg Lys Ser Ser Gly Ser Pro Asp Ser Gln His Cys

645

650

655

Ala Ser Asp Gly Ser Thr Glu Thr Leu Ala Met Val Val Val Glu Pro

660

665

670

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Gly Asp Thr Leu Ser Ser Pro Glu Phe Asp Ser Gly Pro Phe Ser Ser
675 680 685

Gln Ser Asp Glu Thr Ser Leu Ser Thr Thr Ala Ser Ser Ala Thr Pro
690 695 700

Thr Ser Glu Leu Leu Pro Leu Gly Pro Val Asp Gly Arg Ser Cys Ser
705 710 715 720

Met Asp Ser Ala Tyr Gly Thr Leu Ser Pro Thr Ser Leu Gln Asp Phe
725 730 735

Val Ala Pro Gly Pro Met Ala Glu Leu Val Pro Arg Ala Pro Glu Ser
740 745 750

Pro Arg Val Pro Ser Pro Pro Pro Ser Pro Arg Leu Arg Arg Arg Thr
755 760 765

Pro Val Gln Leu Leu Ser Cys Pro Pro His Leu Leu Lys Ser Lys Ser
770 775 780

Glu Ala Ser Leu Leu Gln Leu Leu Ala Gly Ala Gly Thr His Gly Thr
785 790 795 800

Pro Ser Ala Pro Ser Arg Ser Leu Ser Glu Leu Cys Leu Ala Val Pro
805 810 815

Ala Pro Gly Ile Arg Thr Gln Gly Ser Pro Gln Glu Ala Gly Pro Ser
585/735

agatgaagac cagggagagg aaaggggtgga cctgaggccc ccatggagaa gggacgggca 60

ggatgtatgt caccacgccg actgccagca gctgcaccgc cgggggcccc tcaacctctg 120

cgaggcctgt gacagcaagt tccacagcac c atg cat tat gat ggg cat gtc 172

Met His Tyr Asp Gly His Val

1

5

cgc ttc gac ctt ccc cca caa ggc tct gtg ctg gcc cgg aac gtg tcc 220

Arg Phe Asp Leu Pro Pro Gln Gly Ser Val Leu Ala Arg Asn Val Ser

10

15

20

acc cgg tca tgc ccg ccg cgc acc agc ccc gca gtg gac ttg gag gag 268

Thr Arg Ser Cys Pro Pro Arg Thr Ser Pro Ala Val Asp Leu Glu Glu

25

30

35

gag gag gag gag agc tct gtg gat ggc aaa ggg gac cgg aag agc aca 316

Glu Glu Glu Glu Ser Ser Val Asp Gly Lys Gly Asp Arg Lys Ser Thr

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45

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55

ggc ctg aaa ctc tcc aag aag aaa gca agg agg aga cac acg gat gac 364

Gly Leu Lys Leu Ser Lys Lys Lys Ala Arg Arg Arg His Thr Asp Asp

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65

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cca agc aag gaa tgc ttc act ctg aaa ttt gac ctg aat gtg gac att 412

Pro Ser Lys Glu Cys Phe Thr Leu Lys Phe Asp Leu Asn Val Asp Ile

75

80

85

gag aca gag atc gtc cca gcc atg aag aag aag tca ctg ggg gag gtg 460

587/735

Glu Thr Glu Ile Val Pro Ala Met Lys Lys Lys Ser Leu Gly Glu Val

90

95

100

ctg ctg cct gta ttt gaa agg aag ggc att gcg ctg ggc aaa gtg gac 508

Leu Leu Pro Val Phe Glu Arg Lys Gly Ile Ala Leu Gly Lys Val Asp

105

110

115

atc tac ctg gac cag tcc aac aca ccc ctg tcc ctc acc ttc gag gcc 556

Ile Tyr Leu Asp Gln Ser Asn Thr Pro Leu Ser Leu Thr Phe Glu Ala

120

125

130

135

tac agg ttc ggg gga cac tac ctt cgt gtc aaa gcc cca gcc aag cct 604

Tyr Arg Phe Gly Gly His Tyr Leu Arg Val Lys Ala Pro Ala Lys Pro

140

145

150

gga gat gag ggc aag gtg gag cag ggc atg aag gac tcc aag tcc ctg 652

Gly Asp Glu Gly Lys Val Glu Gln Gly Met Lys Asp Ser Lys Ser Leu

155

160

165

agt ttg ccg att ctg cgg cca gct ggg acc ggg ccc ccc gcc ctg gag 700

Ser Leu Pro Ile Leu Arg Pro Ala Gly Thr Gly Pro Pro Ala Leu Glu

170

175

180

cgt gtg gac gcc cag agc cgc cgg gag agc ctg gac atc ttg gcc cct 748

Arg Val Asp Ala Gln Ser Arg Arg Glu Ser Leu Asp Ile Leu Ala Pro

185

190

195

ggc cgc cgc cgc aag aac atg tcg gag ttc ctg ggg gag gcg agc atc 796

Gly Arg Arg Arg Lys Asn Met Ser Glu Phe Leu Gly Glu Ala Ser Ile

| | | | | |
|-----------------------------------------------------------------|-----|-----|-----|------|
| 200 | 205 | 210 | 215 | |
| ccc ggg cag gag ccc ccc acg ccc tcc agc tgc tct ctg ccc agc ggc | | | | 844 |
| Pro Gly Gln Glu Pro Pro Thr Pro Ser Ser Cys Ser Leu Pro Ser Gly | | | | |
| 220 | 225 | 230 | | |
| agc agt ggc agc acc aac act ggc gac agc tgg aag aac cgg gcg gcc | | | | 892 |
| Ser Ser Gly Ser Thr Asn Thr Gly Asp Ser Trp Lys Asn Arg Ala Ala | | | | |
| 235 | 240 | 245 | | |
| agt cgc ttc agc ggc ttt ttc agc tcc ggc ccc agc acc agc gcc ttt | | | | 940 |
| Ser Arg Phe Ser Gly Phe Phe Ser Ser Gly Pro Ser Thr Ser Ala Phe | | | | |
| 250 | 255 | 260 | | |
| ggc cgg gag gta gac aag atg gag cag ctg gag ggc aag ctg cac acc | | | | 988 |
| Gly Arg Glu Val Asp Lys Met Glu Gln Leu Glu Gly Lys Leu His Thr | | | | |
| 265 | 270 | 275 | | |
| tac agc ctc ttc ggg ctg ccc agg ctg ccc cgg ggg ctg cgc ttc gac | | | | 1036 |
| Tyr Ser Leu Phe Gly Leu Pro Arg Leu Pro Arg Gly Leu Arg Phe Asp | | | | |
| 280 | 285 | 290 | 295 | |
| cat gac tcc tgg gag gag gag tac gat gaa gac gag gat gag gac aat | | | | 1084 |
| His Asp Ser Trp Glu Glu Glu Tyr Asp Glu Asp Glu Asp Glu Asp Asn | | | | |
| 300 | 305 | 310 | | |
| gcc tgc ctg agg ctg gag gac agc tgg cgg gag ctc att gat ggg cat | | | | 1132 |
| Ala Cys Leu Arg Leu Glu Asp Ser Trp Arg Glu Leu Ile Asp Gly His | | | | |
| 315 | 320 | 325 | | |
| 589/735 | | | | |

gag aag ctg acc cgg cgg cag tgc cac cag cag gag gcg gtg tgg gag 1180

Glu Lys Leu Thr Arg Arg Gln Cys His Gln Gln Glu Ala Val Trp Glu

330

335

340

ctg ctg cac acg gag gcc tcc tac atc agg aaa ctg cgg gtg atc atc 1228

Leu Leu His Thr Glu Ala Ser Tyr Ile Arg Lys Leu Arg Val Ile Ile

345

350

355

aac ctg ttc ctg tgc tgc ctc ctg aac ctg caa gag tca ggg ctg ctg 1276

Asn Leu Phe Leu Cys Cys Leu Leu Asn Leu Gln Glu Ser Gly Leu Leu

360

365

370

375

tgt gag gtg gag gcg gag cgc ctg ttc agc aac atc ccg gag atc gcg 1324

Cys Glu Val Glu Ala Glu Arg Leu Phe Ser Asn Ile Pro Glu Ile Ala

380

385

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cag ctg cac cgc agg ctg tgg gct agc gtg atg gcg ccg gtg ctg gag 1372

Gln Leu His Arg Arg Leu Trp Ala Ser Val Met Ala Pro Val Leu Glu

395

400

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aag gcg cgg cgc acg cga gcg ctg cta cag ccc ggg gac ttc ctc aaa 1420

Lys Ala Arg Arg Thr Arg Ala Leu Leu Gln Pro Gly Asp Phe Leu Lys

410

415

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ggc ttc aag atg ttc ggc tgc ctc ttc aag ccc tac atc cgc tac tgc 1468

Gly Phe Lys Met Phe Gly Ser Leu Phe Lys Pro Tyr Ile Arg Tyr Cys

425

430

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Met Glu Glu Glu Gly Cys Met Glu Tyr Met Arg Gly Leu Leu Arg Asp

440 445 450 455

aac gac ctc ttc cgg gcc tac atc acg tgg gcg gag aag cac cca cag 1564

Asn Asp Leu Phe Arg Ala Tyr Ile Thr Trp Ala Glu Lys His Pro Gln

460 465 470

tgc cag agg ctg aag ctg agc gac atg ctg gcc aaa ccc cac cag cgg 1612

Cys Gln Arg Leu Lys Leu Ser Asp Met Leu Ala Lys Pro His Gln Arg

475 480 485

ctc acc aag tac ccg ctg ctg ctc aag tcg gtg ctg agg aag acc gag 1660

Leu Thr Lys Tyr Pro Leu Leu Leu Lys Ser Val Leu Arg Lys Thr Glu

490 495 500

gag ccg cgc gcc aag gag gcc gtc gtc gcc atg atc ggc tcc gtg gag 1708

Glu Pro Arg Ala Lys Glu Ala Val Val Ala Met Ile Gly Ser Val Glu

505 510 515

cgc ttc atc cac cac gtg aac gcg tgc atg cgg cag cgg cag gag cgg 1756

Arg Phe Ile His His Val Asn Ala Cys Met Arg Gln Arg Gln Glu Arg

520 525 530 535

cag cgg ctg gcg gcc gtg gtg agc cgc atc gac gcc tac gag gtg gtg 1804

Gln Arg Leu Ala Ala Val Val Ser Arg Ile Asp Ala Tyr Glu Val Val

540 545 550

gaa agc agc agc gac gaa gtg gac aag ctc ctg aag gaa ttt ctg cac 1852

Glu Ser Ser Ser Asp Glu Val Asp Lys Leu Leu Lys Glu Phe Leu His

555

560

565

ctg gac ttg aca gcg ccc atc cct ggc gcc tcc ccg gag gag acg cgg 1900

Leu Asp Leu Thr Ala Pro Ile Pro Gly Ala Ser Pro Glu Glu Thr Arg

570

575

580

cag ctg ctg ctg gag ggg agc ctg agg atg aag gag ggg aag gac agc 1948

Gln Leu Leu Leu Glu Gly Ser Leu Arg Met Lys Glu Gly Lys Asp Ser

585

590

595

aag atg gat gtg tac tgc ttc ctc ttc acg gat ctg ctg ttg gtg acc 1996

Lys Met Asp Val Tyr Cys Phe Leu Phe Thr Asp Leu Leu Leu Val Thr

600

605

610

615

aaa gca gtg aag aag gca gag agg acc agg gtc atc agg cca ccc ctg 2044

Lys Ala Val Lys Lys Ala Glu Arg Thr Arg Val Ile Arg Pro Pro Leu

620

625

630

ctc gtg gac aag att gtg tgc cgg gag cta cgg gac cct ggg tcc ttc 2092

Leu Val Asp Lys Ile Val Cys Arg Glu Leu Arg Asp Pro Gly Ser Phe

635

640

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ctc ctt atc tac ctg aat gag ttt cac agt gct gta ggg gcc tac acg 2140

Leu Leu Ile Tyr Leu Asn Glu Phe His Ser Ala Val Gly Ala Tyr Thr

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ttc cag gcc agt ggc cag gcc ttg tgc cgt ggc tgg gtg gac acc att 2188

Phe Gln Ala Ser Gly Gln Ala Leu Cys Arg Gly Trp Val Asp Thr Ile

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665

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675

tac aat gcc cag aac cag ctg caa cag ctg cgt gca cag gag ccc cca 2236

Tyr Asn Ala Gln Asn Gln Leu Gln Gln Leu Arg Ala Gln Glu Pro Pro

680

685

690

695

ggc agt cag cag ccc ctg cag agc ctg gaa gag gag gag gat gag cag 2284

Gly Ser Gln Gln Pro Leu Gln Ser Leu Glu Glu Glu Glu Asp Glu Gln

700

705

710

gag gag gaa gag gag gag gag gag gag gag gaa ggc gag gac agt 2332

Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Gly Glu Asp Ser

715

720

725

ggc act tca gct gcc agc tcc cct acc atc atg cgg aaa agc agc ggc 2380

Gly Thr Ser Ala Ala Ser Ser Pro Thr Ile Met Arg Lys Ser Ser Gly

730

735

740

agc ccc gac tct cag cac tgt gcc tca gat ggc tcc acg gag acc ctg 2428

Ser Pro Asp Ser Gln His Cys Ala Ser Asp Gly Ser Thr Glu Thr Leu

745

750

755

gcc atg gtt gtg gta gag cct ggg gac acg ctg tcc tcc ccc gag ttc 2476

Ala Met Val Val Val Glu Pro Gly Asp Thr Leu Ser Ser Pro Glu Phe

760

765

770

775

gac agc ggt cct ttc agc tcc cag tct gat gag acc tct ctc agc acc 2524

Asp Ser Gly Pro Phe Ser Ser Gln Ser Asp Glu Thr Ser Leu Ser Thr

780

785

790

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act gcc tca tct gcc acg ccc acc agt gag ctg ctg ccc ctg ggt ccg 2572

Thr Ala Ser Ser Ala Thr Pro Thr Ser Glu Leu Leu Pro Leu Gly Pro

795

800

805

gtg gac ggc cgc tcc tgc tcc atg gac tct gcc tac ggc acc ctc tcc 2620

Val Asp Gly Arg Ser Cys Ser Met Asp Ser Ala Tyr Gly Thr Leu Ser

810

815

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cca acc tcc tta caa gac ttt gtg gcc cca ggc cca atg gca gag cta 2668

Pro Thr Ser Leu Gln Asp Phe Val Ala Pro Gly Pro Met Ala Glu Leu

825

830

835

gtg cct cgg gcc cca gag tcc cca cga gtt cct tcc cct cca ccc tcg 2716

Val Pro Arg Ala Pro Glu Ser Pro Arg Val Pro Ser Pro Pro Pro Ser

840

845

850

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ccc cgt ctc cgc cgc cgc acc cct gtc cag ctg ttg agc tgc ccg ccc 2764

Pro Arg Leu Arg Arg Arg Thr Pro Val Gln Leu Leu Ser Cys Pro Pro

860

865

870

cac ctg ctc aag tct aag tcc gag gcc agc ctc ctc cag ctg ctg gca 2812

His Leu Leu Lys Ser Lys Ser Glu Ala Ser Leu Leu Gln Leu Leu Ala

875

880

885

ggg gct ggc acc cat ggg aca ccc tct gcc ccc agc cgc agc ctg tca 2860

Gly Ala Gly Thr His Gly Thr Pro Ser Ala Pro Ser Arg Ser Leu Ser

890

895

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gag ctc tgc ctg gct gtt cca gcc cca ggt att agg act cag ggc tcc 2908

Glu Leu Cys Leu Ala Val Pro Ala Pro Gly Ile Arg Thr Gln Gly Ser

905

910

915

cct cag gaa gct ggg ccc agc tgg gat tgc cga ggg gcc cct agc cct 2956

Pro Gln Glu Ala Gly Pro Ser Trp Asp Cys Arg Gly Ala Pro Ser Pro

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925

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935

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Gly Ser Gly Pro Gly Leu Val Gly Cys Leu Ala Gly Glu Pro Ala Gly

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tcc cac agg aag agg tgt gga gac ctg ccc tcg ggg gcc tct ccc agg 3052

Ser His Arg Lys Arg Cys Gly Asp Leu Pro Ser Gly Ala Ser Pro Arg

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gtc cag cct gag ccc cca cca ggg gtc tct gcc cag cac agg aag ctg 3100

Val Gln Pro Glu Pro Pro Pro Gly Val Ser Ala Gln His Arg Lys Leu

970

975

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acc ctg gcc cag ctc tac cga atc agg acc acc ctg ctg ctt aac tcc 3148

Thr Leu Ala Gln Leu Tyr Arg Ile Arg Thr Thr Leu Leu Leu Asn Ser

985

990

995

acg ctc act gcc tcg gag gtc tgagcagagg gagggcccca agagtgccat 3199

Thr Leu Thr Ala Ser Glu Val

1000

1005

tgaccaagag acagcagaca gcctgcctcc tggggcgtgc cggcacctgc ttcagctact 3259

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gcctcctgta tgcattgagcc ggatgctggg caggatccct gcctacgccc gggcccgatt 3319

tgcgctttgc cggactggat ggagtggagg aggcccagge cacagtacca cccacactgc 3379

ccaggcagcc cctcgtcacc tactccccga agttaccage tcagctcgag tcttcagggc 3439

tgggctecta ggctgcccatt cctacttcta cctcactgg cctccagtgg gattcactcc 3499

tgccctgccc ccaccttccc agtcccacag gccacccctg gcttgggctg ggttctgtga 3559

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<210> 158

<211> 1006

<212> PRT

<213> Homo sapiens

<400> 158

Met His Tyr Asp Gly His Val Arg Phe Asp Leu Pro Pro Gln Gly Ser

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Val Leu Ala Arg Asn Val Ser Thr Arg Ser Cys Pro Pro Arg Thr Ser

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Pro Ala Val Asp Leu Glu Glu Glu Glu Glu Ser Ser Val Asp Gly

35 40 45

Lys Gly Asp Arg Lys Ser Thr Gly Leu Lys Leu Ser Lys Lys Lys Ala
50 55 60

Arg Arg Arg His Thr Asp Asp Pro Ser Lys Glu Cys Phe Thr Leu Lys
65 70 75 80

Phe Asp Leu Asn Val Asp Ile Glu Thr Glu Ile Val Pro Ala Met Lys
85 90 95

Lys Lys Ser Leu Gly Glu Val Leu Leu Pro Val Phe Glu Arg Lys Gly
100 105 110

Ile Ala Leu Gly Lys Val Asp Ile Tyr Leu Asp Gln Ser Asn Thr Pro
115 120 125

Leu Ser Leu Thr Phe Glu Ala Tyr Arg Phe Gly Gly His Tyr Leu Arg
130 135 140

Val Lys Ala Pro Ala Lys Pro Gly Asp Glu Gly Lys Val Glu Gln Gly
145 150 155 160

Met Lys Asp Ser Lys Ser Leu Ser Leu Pro Ile Leu Arg Pro Ala Gly
165 170 175

Thr Gly Pro Pro Ala Leu Glu Arg Val Asp Ala Gln Ser Arg Arg Glu
180 185 190

Ser Leu Asp Ile Leu Ala Pro Gly Arg Arg Arg Lys Asn Met Ser Glu
195 200 205

Phe Leu Gly Glu Ala Ser Ile Pro Gly Gln Glu Pro Pro Thr Pro Ser

210

215

220

Ser Cys Ser Leu Pro Ser Gly Ser Ser Gly Ser Thr Asn Thr Gly Asp

225

230

235

240

Ser Trp Lys Asn Arg Ala Ala Ser Arg Phe Ser Gly Phe Phe Ser Ser

245

250

255

Gly Pro Ser Thr Ser Ala Phe Gly Arg Glu Val Asp Lys Met Glu Gln

260

265

270

Leu Glu Gly Lys Leu His Thr Tyr Ser Leu Phe Gly Leu Pro Arg Leu

275

280

285

Pro Arg Gly Leu Arg Phe Asp His Asp Ser Trp Glu Glu Glu Tyr Asp

290

295

300

Glu Asp Glu Asp Glu Asp Asn Ala Cys Leu Arg Leu Glu Asp Ser Trp

305

310

315

320

Arg Glu Leu Ile Asp Gly His Glu Lys Leu Thr Arg Arg Gln Cys His

325

330

335

Gln Gln Glu Ala Val Trp Glu Leu Leu His Thr Glu Ala Ser Tyr Ile

340

345

350

Arg Lys Leu Arg Val Ile Ile Asn Leu Phe Leu Cys Cys Leu Leu Asn

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| | | |
|-----------------------------------------------------------------|-----|-----|
| 355 | 360 | 365 |
| Leu Gln Glu Ser Gly Leu Leu Cys Glu Val Glu Ala Glu Arg Leu Phe | | |
| 370 | 375 | 380 |
| Ser Asn Ile Pro Glu Ile Ala Gln Leu His Arg Arg Leu Trp Ala Ser | | |
| 385 | 390 | 395 |
| 400 | | |
| Val Met Ala Pro Val Leu Glu Lys Ala Arg Arg Thr Arg Ala Leu Leu | | |
| 405 | 410 | 415 |
| Gln Pro Gly Asp Phe Leu Lys Gly Phe Lys Met Phe Gly Ser Leu Phe | | |
| 420 | 425 | 430 |
| Lys Pro Tyr Ile Arg Tyr Cys Met Glu Glu Glu Gly Cys Met Glu Tyr | | |
| 435 | 440 | 445 |
| Met Arg Gly Leu Leu Arg Asp Asn Asp Leu Phe Arg Ala Tyr Ile Thr | | |
| 450 | 455 | 460 |
| Trp Ala Glu Lys His Pro Gln Cys Gln Arg Leu Lys Leu Ser Asp Met | | |
| 465 | 470 | 475 |
| 480 | | |
| Leu Ala Lys Pro His Gln Arg Leu Thr Lys Tyr Pro Leu Leu Leu Lys | | |
| 485 | 490 | 495 |
| Ser Val Leu Arg Lys Thr Glu Glu Pro Arg Ala Lys Glu Ala Val Val | | |
| 500 | 505 | 510 |

Ala Met Ile Gly Ser Val Glu Arg Phe Ile His His Val Asn Ala Cys

515

520

525

Met Arg Gln Arg Gln Glu Arg Gln Arg Leu Ala Ala Val Val Ser Arg

530

535

540

Ile Asp Ala Tyr Glu Val Val Glu Ser Ser Ser Asp Glu Val Asp Lys

545

550

555

560

Leu Leu Lys Glu Phe Leu His Leu Asp Leu Thr Ala Pro Ile Pro Gly

565

570

575

Ala Ser Pro Glu Glu Thr Arg Gln Leu Leu Leu Glu Gly Ser Leu Arg

580

585

590

Met Lys Glu Gly Lys Asp Ser Lys Met Asp Val Tyr Cys Phe Leu Phe

595

600

605

Thr Asp Leu Leu Leu Val Thr Lys Ala Val Lys Lys Ala Glu Arg Thr

610

615

620

Arg Val Ile Arg Pro Pro Leu Leu Val Asp Lys Ile Val Cys Arg Glu

625

630

635

640

Leu Arg Asp Pro Gly Ser Phe Leu Leu Ile Tyr Leu Asn Glu Phe His

645

650

655

Ser Ala Val Gly Ala Tyr Thr Phe Gln Ala Ser Gly Gln Ala Leu Cys

660

665

670

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Arg Gly Trp Val Asp Thr Ile Tyr Asn Ala Gln Asn Gln Leu Gln Gln

675

680

685

Leu Arg Ala Gln Glu Pro Pro Gly Ser Gln Gln Pro Leu Gln Ser Leu

690

695

700

Glu Glu Glu Glu Asp Glu Gln Glu Glu Glu Glu Glu Glu Glu Glu

705

710

715

720

Glu Glu Glu Gly Glu Asp Ser Gly Thr Ser Ala Ala Ser Ser Pro Thr

725

730

735

Ile Met Arg Lys Ser Ser Gly Ser Pro Asp Ser Gln His Cys Ala Ser

740

745

750

Asp Gly Ser Thr Glu Thr Leu Ala Met Val Val Val Glu Pro Gly Asp

755

760

765

Thr Leu Ser Ser Pro Glu Phe Asp Ser Gly Pro Phe Ser Ser Gln Ser

770

775

780

Asp Glu Thr Ser Leu Ser Thr Thr Ala Ser Ser Ala Thr Pro Thr Ser

785

790

795

800

Glu Leu Leu Pro Leu Gly Pro Val Asp Gly Arg Ser Cys Ser Met Asp

805

810

815

Ser Ala Tyr Gly Thr Leu Ser Pro Thr Ser Leu Gln Asp Phe Val Ala

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..

820

825

830

Pro Gly Pro Met Ala Glu Leu Val Pro Arg Ala Pro Glu Ser Pro Arg

835

840

845

Val Pro Ser Pro Pro Pro Ser Pro Arg Leu Arg Arg Arg Thr Pro Val

850

855

860

Gln Leu Leu Ser Cys Pro Pro His Leu Leu Lys Ser Lys Ser Glu Ala

865

870

875

880

Ser Leu Leu Gln Leu Leu Ala Gly Ala Gly Thr His Gly Thr Pro Ser

885

890

895

Ala Pro Ser Arg Ser Leu Ser Glu Leu Cys Leu Ala Val Pro Ala Pro

900

905

910

Gly Ile Arg Thr Gln Gly Ser Pro Gln Glu Ala Gly Pro Ser Trp Asp

915

920

925

Cys Arg Gly Ala Pro Ser Pro Gly Ser Gly Pro Gly Leu Val Gly Cys

930

935

940

Leu Ala Gly Glu Pro Ala Gly Ser His Arg Lys Arg Cys Gly Asp Leu

945

950

955

960

Pro Ser Gly Ala Ser Pro Arg Val Gln Pro Glu Pro Pro Pro Gly Val

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970

975

THE UNIVERSITY OF CHICAGO

985



1000

1005

<212> DNA

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<222> (93).. (3089)

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Met Gly Trp Lys Pro Ser Glu

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Ala Arg Gly Gln Ser Gln Ser Leu Gln Ala Ser Gly Leu Gln Pro Arg

15

20

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Ser Leu Lys Ala Ala Arg Arg Ala Thr Gly Arg Pro Asp Arg Ser Arg

25

30

35

gca gcc ccg ccc aac atg gac cca gac ccc cag gcg ggc gtg cag gtg 257

Ala Ala Pro Pro Asn Met Asp Pro Asp Pro Gln Ala Gly Val Gln Val

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45

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ggc atg cgg gtg gtg cgc ggc gtg gac tgg aag tgg ggc cag cag gac 305

Gly Met Arg Val Val Arg Gly Val Asp Trp Lys Trp Gly Gln Gln Asp

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ggc ggc gag ggc ggc gtg ggc acg gtg gtg gag ctt ggc cgc cac ggc 353

Gly Gly Glu Gly Gly Val Gly Thr Val Val Glu Leu Gly Arg His Gly

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80

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agc ccc tcg aca ccc gac cgc aca gtg gtc gtg cag tgg gac cag ggc 401

Ser Pro Ser Thr Pro Asp Arg Thr Val Val Val Gln Trp Asp Gln Gly

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acg cgc acc aac tac cgc gcc ggc tac cag ggc gcg cac gac ctg ctg 449

Thr Arg Thr Asn Tyr Arg Ala Gly Tyr Gln Gly Ala His Asp Leu Leu

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ctg tac gac aac gcc cag atc ggc gtc cgg cac ccc aac atc atc tgt 497

Leu Tyr Asp Asn Ala Gln Ile Gly Val Arg His Pro Asn Ile Ile Cys

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gac tgc tgc aag aag cac ggg ctg cgg ggg atg cgc tgg aag tgc cgt 545

Asp Cys Cys Lys Lys His Gly Leu Arg Gly Met Arg Trp Lys Cys Arg

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gtg tgc ctg gac tac gac ctc tgc acg cag tgc tac atg cac aac aag 593

Val Cys Leu Asp Tyr Asp Leu Cys Thr Gln Cys Tyr Met His Asn Lys

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cat gag ctc gcc cac gcc ttc gac cgc tac gag acc gct cac tcg cgc 641

His Glu Leu Ala His Ala Phe Asp Arg Tyr Glu Thr Ala His Ser Arg

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cct gtc aca ctg agt ccc cgc cag ggc ctc ccg agg atc cca cta agg 689

Pro Val Thr Leu Ser Pro Arg Gln Gly Leu Pro Arg Ile Pro Leu Arg

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ggc atc ttc cag gga gcg aag gtg gtg cga ggc ccc ttc tgg gag tgg 737

Gly Ile Phe Gln Gly Ala Lys Val Val Arg Gly Pro Phe Trp Glu Trp

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ggc tca cag gat gga ggg gaa ggg aaa ccg ggc cgt gtg gtg gac atc 785

Gly Ser Gln Asp Gly Gly Glu Gly Lys Pro Gly Arg Val Val Asp Ile

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cgt ggc tgg gat gtg gag aca ggc cgg agt gtg gcc agc gtg acg tgg 833

Arg Gly Trp Asp Val Glu Thr Gly Arg Ser Val Ala Ser Val Thr Trp

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gct gat ggt acc acc aat gtg tac cgt gtg ggc cac aag ggc aag gtg 881

Ala Asp Gly Thr Thr Asn Val Tyr Arg Val Gly His Lys Gly Lys Val

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gac ctc aag tgt gtg ggc gag gca gcg ggc ggc ttc tac tac aag gac 929

Asp Leu Lys Cys Val Gly Glu Ala Ala Gly Gly Phe Tyr Tyr Lys Asp

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cac ctc cca agg ctc ggc aag ccg gcg gag ctg cag cgc agg gtg agt 977

His Leu Pro Arg Leu Gly Lys Pro Ala Glu Leu Gln Arg Arg Val Ser

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gct gac agc cag ccc ttc cag cac ggg gac aag gtc aag tgt ctg ctg 1025

Ala Asp Ser Gln Pro Phe Gln His Gly Asp Lys Val Lys Cys Leu Leu

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gac act gat gtc ctg cgg gag atg cag gaa ggc cac ggc ggc tgg aac 1073

Asp Thr Asp Val Leu Arg Glu Met Gln Glu Gly His Gly Gly Trp Asn

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ccc agg atg gcg gag ttt atc gga cag acg ggc acc gtg cat cgt atc 1121

Pro Arg Met Ala Glu Phe Ile Gly Gln Thr Gly Thr Val His Arg Ile

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acg gac cgc ggg gac gtg cgc gtg cag ttc aac cac gag acg cgc tgg 1169

Thr Asp Arg Gly Asp Val Arg Val Gln Phe Asn His Glu Thr Arg Trp

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acc ttc cac ccc ggg gcg ctc acc aag cac cac tcc ttc tgg gtg ggc 1217

Thr Phe His Pro Gly Ala Leu Thr Lys His His Ser Phe Trp Val Gly

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gac gtg gtc cgg gtc atc ggc gac ctt gac aca gtg aag cgg ctg cag 1265

Asp Val Val Arg Val Ile Gly Asp Leu Asp Thr Val Lys Arg Leu Gln

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Ala Gly His Gly Glu Trp Thr Asp Asp Met Ala Pro Ala Leu Gly Arg

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Val Gly Lys Val Val Lys Val Phe Gly Asp Gly Asn Leu Arg Val Ala

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Val Ala Gly Gln Arg Trp Thr Phe Ser Pro Ser Cys Leu Val Ala Tyr

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Asn Lys Ser Ser Leu Ser Val Ala Leu Asp Lys Leu Arg Ala Gln Lys

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agt gac cca gag cac ccg gga agg ctg gtg gtg gag gtg gcg ctg ggt 1553

Ser Asp Pro Glu His Pro Gly Arg Leu Val Val Glu Val Ala Leu Gly

475

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aac gca gcc cgg gct ctg gac ctg ctg cgg agg cgc cca gag caa gtg 1601

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Asn Ala Ala Arg Ala Leu Asp Leu Leu Arg Arg Arg Pro Glu Gln Val

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gac acc aag aac caa ggc agg acc gct ctg caa gtg gct gcc tac ctg 1649

Asp Thr Lys Asn Gln Gly Arg Thr Ala Leu Gln Val Ala Ala Tyr Leu

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Gly Gln Val Glu Leu Ile Arg Leu Leu Leu Gln Ala Arg Ala Gly Val

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Gly Asn Gln Pro Glu Ala Thr Arg Val Leu Leu Ser Ala Gly Cys Arg

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Ala Asp Ala Ile Asn Ser Thr Gln Ser Thr Ala Leu His Val Ala Val

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cag agg ggc ttc ctg gag gtg gtg cgg gcc ctg tgt gag cgc ggc tgt 1889

Gln Arg Gly Phe Leu Glu Val Val Arg Ala Leu Cys Glu Arg Gly Cys

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gac gtc aac ctg ccc gac gcc cac tcg gac acg ccc ctg cac tcc gcc 1937

Asp Val Asn Leu Pro Asp Ala His Ser Asp Thr Pro Leu His Ser Ala

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600 605 610 615
 atc tgc ggc act gga gcc agc ggc att gtc gag gtc ctc acg gag 1985
 Ile Ser Ala Gly Thr Gly Ala Ser Gly Ile Val Glu Val Leu Thr Glu
 620 625 630

gtg cca aac atc gat gtt acc gcc acc aac agc cag ggt ttc acc ctg 2033
 Val Pro Asn Ile Asp Val Thr Ala Thr Asn Ser Gln Gly Phe Thr Leu
 635 640 645

ctg cac cat gcc tcc ctc aag ggt cac gcg cta gct gtg aga aag att 2081
 Leu His His Ala Ser Leu Lys Gly His Ala Leu Ala Val Arg Lys Ile
 650 655 660

ctg gct cgg gcg cgg cag ctg gtg gac gcc aag aag gag gac ggc ttc 2129
 Leu Ala Arg Ala Arg Gln Leu Val Asp Ala Lys Lys Glu Asp Gly Phe
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 Thr Ala Leu His Leu Ala Ala Leu Asn Asn His Arg Glu Val Ala Gln
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 Leu Gln Ser Pro Leu His Leu Ala Val Gln Gln Ala His Val Gly Leu
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Val Pro Leu Leu Val Asp Ala Gly Cys Ser Val Asn Ala Glu Asp Glu

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gag ggg gac aca gcc ctg cac gtg gcg ctg cag cgt cat cag ctg ctg 2369

Glu Gly Asp Thr Ala Leu His Val Ala Leu Gln Arg His Gln Leu Leu

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ccc ctg gtg gct gat ggg gcc ggg ggg gac cca ggg ccc ttg cag ctg 2417

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765

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ctg tcc agg cta cag gcc tcg ggc ctc ccc ggc agc gcg gag ctg acg 2465

Leu Ser Arg Leu Gln Ala Ser Gly Leu Pro Gly Ser Ala Glu Leu Thr

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785

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gtg ggc gcg gcg gtc gcc tgc ttc ctg gcg ctg gag ggc gcc gac gtg 2513

Val Gly Ala Ala Val Ala Cys Phe Leu Ala Leu Glu Gly Ala Asp Val

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Ser Tyr Thr Asn His Arg Gly Arg Ser Pro Leu Asp Leu Ala Ala Glu

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Gly Arg Val Leu Lys Ala Leu Gln Gly Cys Ala Gln Arg Phe Arg Glu

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cg g cag gcg ggc ggg ggc gcg gcc ccg ggc ccc agg caa acg ctc ggg 2657

Arg Gln Ala Gly Gly Gly Ala Ala Pro Gly Pro Arg Gln Thr Leu Gly

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acc ccc aac acc gtg acg aac ctg cac gtg ggc gcc gcg ccg ggg ccc 2705

Thr Pro Asn Thr Val Thr Asn Leu His Val Gly Ala Ala Pro Gly Pro

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gag gcc gct gag tgc ctg gtg tgc tcc gag ctg gcg ctg ctg gtg ctg 2753

Glu Ala Ala Glu Cys Leu Val Cys Ser Glu Leu Ala Leu Leu Val Leu

875 880 885

ttc tcg ccg tgc cag cac cgc acc gtg tgt gag gag tgc gcg cgc agg 2801

Phe Ser Pro Cys Gln His Arg Thr Val Cys Glu Glu Cys Ala Arg Arg

890 895 900

atg aag aag tgc atc agg tgc cag gtg gtc gtc agc aag aaa ctg cgc 2849

Met Lys Lys Cys Ile Arg Cys Gln Val Val Val Ser Lys Lys Leu Arg

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cca gac ggc tct gag gtg gcg agc gcc gcc ccc gcc ccc ggc ccg ccg 2897

Pro Asp Gly Ser Glu Val Ala Ser Ala Ala Pro Ala Pro Gly Pro Pro

920 925 930 935

cgc cag ctg gtg gag gag ctg cag agc cgc tac cgg cag atg gag gaa 2945

Arg Gln Leu Val Glu Glu Leu Gln Ser Arg Tyr Arg Gln Met Glu Glu

940 945 950

cgc atc acc tgc ccc atc tgc atc gac agg cac atc cgc ctc gtg ttc 2993

Arg Ile Thr Cys Pro Ile Cys Ile Asp Arg His Ile Arg Leu Val Phe

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Gln Cys Gly His Gly Ala Cys Ala Pro Cys Gly Ser Ala Leu Ser Ala

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Cys Pro Ile Cys Arg Gln Pro Ile Arg Asp Arg Ile Gln Ile Phe Val

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3168

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Ala Ser Gly Leu Gln Pro Arg Ser Leu Lys Ala Ala Arg Arg Ala Thr

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Gly Arg Pro Asp Arg Ser Arg Ala Ala Pro Pro Asn Met Asp Pro Asp

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all amino acids are present in the protein

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Pro Gln Ala Gly Val Gln Val Gly Met Arg Val Val Arg Gly Val Asp

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Trp Lys Trp Gly Gln Gln Asp Gly Gly Glu Gly Gly Val Gly Thr Val

65

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80

Val Glu Leu Gly Arg His Gly Ser Pro Ser Thr Pro Asp Arg Thr Val

85

90

95

Val Val Gln Trp Asp Gln Gly Thr Arg Thr Asn Tyr Arg Ala Gly Tyr

100

105

110

Gln Gly Ala His Asp Leu Leu Leu Tyr Asp Asn Ala Gln Ile Gly Val

115

120

125

Arg His Pro Asn Ile Ile Cys Asp Cys Cys Lys Lys His Gly Leu Arg

130

135

140

Gly Met Arg Trp Lys Cys Arg Val Cys Leu Asp Tyr Asp Leu Cys Thr

145

150

155

160

Gln Cys Tyr Met His Asn Lys His Glu Leu Ala His Ala Phe Asp Arg

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Tyr Glu Thr Ala His Ser Arg Pro Val Thr Leu Ser Pro Arg Gln Gly

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THE UNIVERSITY OF CHICAGO

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[REDACTED]

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Phe Asn His Glu Thr Arg Trp Thr Phe His Pro Gly Ala Leu Thr Lys

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360

365

His His Ser Phe Trp Val Gly Asp Val Val Arg Val Ile Gly Asp Leu

370

375

380

Asp Thr Val Lys Arg Leu Gln Ala Gly His Gly Glu Trp Thr Asp Asp

385

390

395

400

Met Ala Pro Ala Leu Gly Arg Val Gly Lys Val Val Lys Val Phe Gly

405

410

415

Asp Gly Asn Leu Arg Val Ala Val Ala Gly Gln Arg Trp Thr Phe Ser

420

425

430

Pro Ser Cys Leu Val Ala Tyr Arg Pro Glu Glu Asp Ala Asn Leu Asp

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440

445

Val Ala Glu Arg Ala Arg Glu Asn Lys Ser Ser Leu Ser Val Ala Leu

450

455

460

Asp Lys Leu Arg Ala Gln Lys Ser Asp Pro Glu His Pro Gly Arg Leu

465

470

475

480

Val Val Glu Val Ala Leu Gly Asn Ala Ala Arg Ala Leu Asp Leu Leu

485

490

495

Arg Arg Arg Pro Glu Gln Val Asp Thr Lys Asn Gln Gly Arg Thr Ala

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.. .. .

500

505

510

Leu Gln Val Ala Ala Tyr Leu Gly Gln Val Glu Leu Ile Arg Leu Leu

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520

525

Leu Gln Ala Arg Ala Gly Val Asp Leu Pro Asp Asp Glu Gly Asn Thr

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Ala Leu His Tyr Ala Ala Leu Gly Asn Gln Pro Glu Ala Thr Arg Val

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560

Leu Leu Ser Ala Gly Cys Arg Ala Asp Ala Ile Asn Ser Thr Gln Ser

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570

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Thr Ala Leu His Val Ala Val Gln Arg Gly Phe Leu Glu Val Val Arg

580

585

590

Ala Leu Cys Glu Arg Gly Cys Asp Val Asn Leu Pro Asp Ala His Ser

595

600

605

Asp Thr Pro Leu His Ser Ala Ile Ser Ala Gly Thr Gly Ala Ser Gly

610

615

620

Ile Val Glu Val Leu Thr Glu Val Pro Asn Ile Asp Val Thr Ala Thr

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630

635

640

Asn Ser Gln Gly Phe Thr Leu Leu His His Ala Ser Leu Lys Gly His

645

650

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Ala Leu Ala Val Arg Lys Ile Leu Ala Arg Ala Arg Gln Leu Val Asp

660

665

670

Ala Lys Lys Glu Asp Gly Phe Thr Ala Leu His Leu Ala Ala Leu Asn

675

680

685

Asn His Arg Glu Val Ala Gln Ile Leu Ile Arg Glu Gly Arg Cys Asp

690

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Val Asn Val Arg Asn Arg Lys Leu Gln Ser Pro Leu His Leu Ala Val

705

710

715

720

Gln Gln Ala His Val Gly Leu Val Pro Leu Leu Val Asp Ala Gly Cys

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735

Ser Val Asn Ala Glu Asp Glu Glu Gly Asp Thr Ala Leu His Val Ala

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750

Leu Gln Arg His Gln Leu Leu Pro Leu Val Ala Asp Gly Ala Gly Gly

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760

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Asp Pro Gly Pro Leu Gln Leu Leu Ser Arg Leu Gln Ala Ser Gly Leu

770

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Pro Gly Ser Ala Glu Leu Thr Val Gly Ala Ala Val Ala Cys Phe Leu

785

790

795

800

Ala Leu Glu Gly Ala Asp Val Ser Tyr Thr Asn His Arg Gly Arg Ser

805

810

815

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Pro Leu Asp Leu Ala Ala Glu Gly Arg Val Leu Lys Ala Leu Gln Gly

820

825

830

Cys Ala Gln Arg Phe Arg Glu Arg Gln Ala Gly Gly Gly Ala Ala Pro

835

840

845

Gly Pro Arg Gln Thr Leu Gly Thr Pro Asn Thr Val Thr Asn Leu His

850

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Val Gly Ala Ala Pro Gly Pro Glu Ala Ala Glu Cys Leu Val Cys Ser

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875

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Glu Leu Ala Leu Leu Val Leu Phe Ser Pro Cys Gln His Arg Thr Val

885

890

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Cys Glu Glu Cys Ala Arg Arg Met Lys Lys Cys Ile Arg Cys Gln Val

900

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Val Val Ser Lys Lys Leu Arg Pro Asp Gly Ser Glu Val Ala Ser Ala

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Ala Pro Ala Pro Gly Pro Pro Arg Gln Leu Val Glu Glu Leu Gln Ser

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Arg Tyr Arg Gln Met Glu Glu Arg Ile Thr Cys Pro Ile Cys Ile Asp

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Arg His Ile Arg Leu Val Phe Gln Cys Gly His Gly Ala Cys Ala Pro

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Ser Leu Lys Ala Ala Arg Arg Ala Thr Gly Arg Pro Asp Arg Ser Arg

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gca gcc ccg ccc aac atg gac cca gac ccc cag gcg ggc gtg cag gtg 257

Ala Ala Pro Pro Asn Met Asp Pro Asp Pro Gln Ala Gly Val Gln Val

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ggc atg cgg gtg gtg cgc ggc gtg gac tgg aag tgg ggc cag cag gac 305

Gly Met Arg Val Val Arg Gly Val Asp Trp Lys Trp Gly Gln Gln Asp

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ggc ggc gag ggc ggc gtg ggc acg gtg gtg gag ctt ggc cgc cac ggc 353

Gly Gly Glu Gly Gly Val Gly Thr Val Val Glu Leu Gly Arg His Gly

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agc ccc tcg aca ccc gac cgc aca gtg gtc gtg cag tgg gac cag ggc 401

Ser Pro Ser Thr Pro Asp Arg Thr Val Val Val Gln Trp Asp Gln Gly

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Thr Arg Thr Asn Tyr Arg Ala Gly Tyr Gln Gly Ala His Asp Leu Leu

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ctg tac gac aac gcc cag atc ggc gtc cgg cac ccc aac atc atc tgt 497

Leu Tyr Asp Asn Ala Gln Ile Gly Val Arg His Pro Asn Ile Ile Cys

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gac tgc tgc aag aag cac ggg ctg cgg ggg atg cgc tgg aag tgc cgt 545

Asp Cys Cys Lys Lys His Gly Leu Arg Gly Met Arg Trp Lys Cys Arg

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gtg tgc ctg gac tac gac ctc tgc acg cag tgc tac atg cac aac aag 593

Val Cys Leu Asp Tyr Asp Leu Cys Thr Gln Cys Tyr Met His Asn Lys

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cat gag ctc gcc cac gcc ttc gac cgc tac gag acc gct cac tgc cgc 641

His Glu Leu Ala His Ala Phe Asp Arg Tyr Glu Thr Ala His Ser Arg

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Pro Val Thr Leu Ser Pro Arg Gln Gly Leu Pro Arg Ile Pro Leu Arg

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ggc atc ttc cag gga gcg aag gtg gtg cga ggc ccc ttc tgg gag tgg 737

Gly Ile Phe Gln Gly Ala Lys Val Val Arg Gly Pro Phe Trp Glu Trp

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ggc tca cag gat gga ggg gaa ggg aaa ccg ggc cgt gtg gtg gac atc 785

Gly Ser Gln Asp Gly Gly Glu Gly Lys Pro Gly Arg Val Val Asp Ile

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Arg Gly Trp Asp Val Glu Thr Gly Arg Ser Val Ala Ser Val Thr Trp

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gct gat ggt acc acc aat gtg tac cgt gtg ggc cac aag ggc aag gtg 881

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Ala Asp Gly Thr Thr Asn Val Tyr Arg Val Gly His Lys Gly Lys Val

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gac ctc aag tgt gtg ggc gag gca gcg ggc ggc ttc tac tac aag gac 929

Asp Leu Lys Cys Val Gly Glu Ala Ala Gly Gly Phe Tyr Tyr Lys Asp

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His Leu Pro Arg Leu Gly Lys Pro Ala Glu Leu Gln Arg Arg Val Ser

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gct gac agc cag ccc ttc cag cac ggg gac aag gtc aag tgt ctg ctg 1025

Ala Asp Ser Gln Pro Phe Gln His Gly Asp Lys Val Lys Cys Leu Leu

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305

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gac act gat gtc ctg cgg gag atg cag gaa ggc cac ggc ggc tgg aac 1073

Asp Thr Asp Val Leu Arg Glu Met Gln Glu Gly His Gly Gly Trp Asn

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ccc agg atg gcg gag ttt atc gga cag acg ggc acc gtg cat cgt atc 1121

Pro Arg Met Ala Glu Phe Ile Gly Gln Thr Gly Thr Val His Arg Ile

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acc ttc cac ccc ggg gcg ctc acc aag cac cac tcc ttc tgg gtg ggc 1217

Thr Phe His Pro Gly Ala Leu Thr Lys His His Ser Phe Trp Val Gly

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| | | | |
|-----------------------------------------------------------------|-----|-----|------|
| 825 | 830 | 835 | |
| cgg cag gcg ggc ggg ggc gcg gcc ccg ggc ccc agg caa acg ctc ggg | | | 2657 |
| Arg Gln Ala Gly Gly Gly Ala Ala Pro Gly Pro Arg Gln Thr Leu Gly | | | |
| 840 | 845 | 850 | 855 |
| acc ccc aac acc gtg acg aac ctg cac gtg ggc gcc gcg ccg ggg ccc | | | 2705 |
| Thr Pro Asn Thr Val Thr Asn Leu His Val Gly Ala Ala Pro Gly Pro | | | |
| | 860 | 865 | 870 |
| gag gcc gct gag tgc ctg gtg tgc tcc gag ctg gcg ctg ctg gtg ctg | | | 2753 |
| Glu Ala Ala Glu Cys Leu Val Cys Ser Glu Leu Ala Leu Leu Val Leu | | | |
| | 875 | 880 | 885 |
| ttc tcg ccg tgc cag cac cgc acc gtg tgt gag gag tgc gcg cgc agg | | | 2801 |
| Phe Ser Pro Cys Gln His Arg Thr Val Cys Glu Glu Cys Ala Arg Arg | | | |
| | 890 | 895 | 900 |
| atg aag aag tgc atc agg tgc cag gtg gtc gtc agc aag aaa ctg cgc | | | 2849 |
| Met Lys Lys Cys Ile Arg Cys Gln Val Val Val Ser Lys Lys Leu Arg | | | |
| | 905 | 910 | 915 |
| cca gac ggc tct gag gtg gcg agc gcc gcc ccc gcc ccc ggc ccg ccg | | | 2897 |
| Pro Asp Gly Ser Glu Val Ala Ser Ala Ala Pro Ala Pro Gly Pro Pro | | | |
| 920 | 925 | 930 | 935 |
| cgc cag ctg gtg gag gag ctg cag agc cgc tac cgg cag atg gag gaa | | | 2945 |
| Arg Gln Leu Val Glu Glu Leu Gln Ser Arg Tyr Arg Gln Met Glu Glu | | | |
| | 940 | 945 | 950 |

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Arg Ile Thr Cys Pro Ile Cys Ile Asp Ser His Ile Arg Leu Val Phe
955 960 965

cag tgc ggc cac ggc gca tgc gcc ccc tgc ggc tcc gcg ctc agc gcc 3041
Gln Cys Gly His Gly Ala Cys Ala Pro Cys Gly Ser Ala Leu Ser Ala
970 975 980

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Cys Pro Ile Cys Arg Gln Pro Ile Arg Asp Arg Ile Gln Ile Phe Val
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Gly Arg Pro Asp Arg Ser Arg Ala Ala Pro Pro Asn Met Asp Pro Asp

35

40

45

Pro Gln Ala Gly Val Gln Val Gly Met Arg Val Val Arg Gly Val Asp

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Trp Lys Trp Gly Gln Gln Asp Gly Gly Glu Gly Gly Val Gly Thr Val

65

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75

80

Val Glu Leu Gly Arg His Gly Ser Pro Ser Thr Pro Asp Arg Thr Val

85

90

95

Val Val Gln Trp Asp Gln Gly Thr Arg Thr Asn Tyr Arg Ala Gly Tyr

100

105

110

Gln Gly Ala His Asp Leu Leu Leu Tyr Asp Asn Ala Gln Ile Gly Val

115

120

125

Arg His Pro Asn Ile Ile Cys Asp Cys Cys Lys Lys His Gly Leu Arg

130

135

140

Gly Met Arg Trp Lys Cys Arg Val Cys Leu Asp Tyr Asp Leu Cys Thr

145

150

155

160

Gln Cys Tyr Met His Asn Lys His Glu Leu Ala His Ala Phe Asp Arg

165

170

175

Tyr Glu Thr Ala His Ser Arg Pro Val Thr Leu Ser Pro Arg Gln Gly

180

185

190

Leu Pro Arg Ile Pro Leu Arg Gly Ile Phe Gln Gly Ala Lys Val Val

195

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205

Arg Gly Pro Phe Trp Glu Trp Gly Ser Gln Asp Gly Gly Glu Gly Lys

210

215

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Pro Gly Arg Val Val Asp Ile Arg Gly Trp Asp Val Glu Thr Gly Arg

225

230

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240

Ser Val Ala Ser Val Thr Trp Ala Asp Gly Thr Thr Asn Val Tyr Arg

245

250

255

Val Gly His Lys Gly Lys Val Asp Leu Lys Cys Val Gly Glu Ala Ala

260

265

270

Gly Gly Phe Tyr Tyr Lys Asp His Leu Pro Arg Leu Gly Lys Pro Ala

275

280

285

Glu Leu Gln Arg Arg Val Ser Ala Asp Ser Gln Pro Phe Gln His Gly

290

295

300

Asp Lys Val Lys Cys Leu Leu Asp Thr Asp Val Leu Arg Glu Met Gln

305

310

315

320

Glu Gly His Gly Gly Trp Asn Pro Arg Met Ala Glu Phe Ile Gly Gln

325

330

335

Thr Gly Thr Val His Arg Ile Thr Asp Arg Gly Asp Val Arg Val Gln
340 345 350

Phe Asn His Glu Thr Arg Trp Thr Phe His Pro Gly Ala Leu Thr Lys
355 360 365

His His Ser Phe Trp Val Gly Asp Val Val Arg Val Ile Gly Asp Leu
370 375 380

Asp Thr Val Lys Arg Leu Gln Ala Gly His Gly Glu Trp Thr Asp Asp
385 390 395 400

Met Ala Pro Ala Leu Gly Arg Val Gly Lys Val Val Lys Val Phe Gly
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Asp Gly Asn Leu Arg Val Ala Val Ala Gly Gln Arg Trp Thr Phe Ser
420 425 430

Pro Ser Cys Leu Val Ala Tyr Arg Pro Glu Glu Asp Ala Asn Leu Asp
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Val Ala Glu Arg Ala Arg Glu Asn Lys Ser Ser Leu Ser Val Ala Leu
450 455 460

Asp Lys Leu Arg Ala Gln Lys Ser Asp Pro Glu His Pro Gly Arg Leu
465 470 475 480

Val Val Glu Val Ala Leu Gly Asn Ala Ala Arg Ala Leu Asp Leu Leu
485 490 495

Arg Arg Arg Pro Glu Gln Val Asp Thr Lys Asn Gln Gly Arg Thr Ala

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Leu Gln Val Ala Ala Tyr Leu Gly Gln Val Glu Leu Ile Arg Leu Leu

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Leu Gln Ala Arg Ala Gly Val Asp Leu Pro Asp Asp Glu Gly Asn Thr

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540

Ala Leu His Tyr Ala Ala Leu Gly Asn Gln Pro Glu Ala Thr Arg Val

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Leu Leu Ser Ala Gly Cys Arg Ala Asp Ala Ile Asn Ser Thr Gln Ser

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Thr Ala Leu His Val Ala Val Gln Arg Gly Phe Leu Glu Val Val Arg

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Ala Leu Cys Glu Arg Gly Cys Asp Val Asn Leu Pro Asp Ala His Ser

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Asp Thr Pro Leu His Ser Ala Ile Ser Ala Gly Thr Gly Ala Ser Gly

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620

Ile Val Glu Val Leu Thr Glu Val Pro Asn Ile Asp Val Thr Ala Thr

625

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Asn Ser Gln Gly Phe Thr Leu Leu His His Ala Ser Leu Lys Gly His

632/735

645

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Ala Leu Ala Val Arg Lys Ile Leu Ala Arg Ala Arg Gln Leu Val Asp

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665

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Ala Lys Lys Glu Asp Gly Phe Thr Ala Leu His Leu Ala Ala Leu Asn

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680

685

Asn His Arg Glu Val Ala Gln Ile Leu Ile Arg Glu Gly Arg Cys Asp

690

695

700

Val Asn Val Arg Asn Arg Lys Leu Gln Ser Pro Leu His Leu Ala Val

705

710

715

720

Gln Gln Ala His Val Gly Leu Val Pro Leu Leu Val Asp Ala Gly Cys

725

730

735

Ser Val Asn Ala Glu Asp Glu Glu Gly Asp Thr Ala Leu His Val Ala

740

745

750

Leu Gln Arg His Gln Leu Leu Pro Leu Val Ala Asp Gly Ala Gly Gly

755

760

765

Asp Pro Gly Pro Leu Gln Leu Leu Ser Arg Leu Gln Ala Ser Gly Leu

770

775

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Pro Gly Ser Ala Glu Leu Thr Val Gly Ala Ala Val Ala Cys Phe Leu

785

790

795

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Pro Leu Asp Leu Ala Ala Glu Gly Arg Val Leu Lys Ala Leu Gln Gly
820 825 830

Cys Ala Gln Arg Phe Arg Glu Arg Gln Ala Gly Gly Gly Ala Ala Pro
835 840 845

Gly Pro Arg Gln Thr Leu Gly Thr Pro Asn Thr Val Thr Asn Leu His
850 855 860

Val Gly Ala Ala Pro Gly Pro Glu Ala Ala Glu Cys Leu Val Cys Ser
865 870 875 880

Glu Leu Ala Leu Leu Val Leu Phe Ser Pro Cys Gln His Arg Thr Val
885 890 895

Cys Glu Glu Cys Ala Arg Arg Met Lys Lys Cys Ile Arg Cys Gln Val
900 905 910

Val Val Ser Lys Lys Leu Arg Pro Asp Gly Ser Glu Val Ala Ser Ala
915 920 925

Ala Pro Ala Pro Gly Pro Pro Arg Gln Leu Val Glu Glu Leu Gln Ser
930 935 940

Arg Tyr Arg Gln Met Glu Glu Arg Ile Thr Cys Pro Ile Cys Ile Asp
945 950 955 960

Ser His Ile Arg Leu Val Phe Gln Cys Gly His Gly Ala Cys Ala Pro

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985

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Met Ile Ala Trp Arg Leu Pro Leu

1

5

tgc gtg ctc ttg gtg gcc tcc gtc gag agc cac ctg ggg gcc ctg ggg 162

635/735

Cys Val Leu Leu Val Ala Ser Val Glu Ser His Leu Gly Ala Leu Gly

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ccc aag aac gtc tcg cag aaa gac gcg gag ttt gag cgc acc tac gcg 210

Pro Lys Asn Val Ser Gln Lys Asp Ala Glu Phe Glu Arg Thr Tyr Ala

25

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35

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gac gac gtc aac agc gag ctg gtc aac atc tac acc ttc aac cac acc 258

Asp Asp Val Asn Ser Glu Leu Val Asn Ile Tyr Thr Phe Asn His Thr

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gtg acc cgc aac cgg acc gag ggt gtg cga gtg tct gtg aat gtc ctg 306

Val Thr Arg Asn Arg Thr Glu Gly Val Arg Val Ser Val Asn Val Leu

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aac aag cag aaa ggg gcg cct ttg ctg ttc gtg gtc cgc cag aag gag 354

Asn Lys Gln Lys Gly Ala Pro Leu Leu Phe Val Val Arg Gln Lys Glu

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gct gtt gtg tcc ttc cag gtg ccc cta atc ctt cga gga ctg tat cag 402

Ala Val Val Ser Phe Gln Val Pro Leu Ile Leu Arg Gly Leu Tyr Gln

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cgg aag tac ctc tac caa aaa gtg gaa cga act ctg tgt cag ccc ccc 450

Arg Lys Tyr Leu Tyr Gln Lys Val Glu Arg Thr Leu Cys Gln Pro Pro

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acc aag aat gag tct gag atc cag ttt ttc tat gtg gac gtg tct acc 498

Thr Lys Asn Glu Ser Glu Ile Gln Phe Phe Tyr Val Asp Val Ser Thr

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ctg tca ccc gtc aat acc act tac cag ctc cga gtc aac cgt gtg gac 546
Leu Ser Pro Val Asn Thr Thr Tyr Gln Leu Arg Val Asn Arg Val Asp

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gcc cag ccc cag tac ttc aaa tac gag ttt cct gat ggt gtg gac tcg 642
Ala Gln Pro Gln Tyr Phe Lys Tyr Glu Phe Pro Asp Gly Val Asp Ser

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gta att gtc aag gtg acc tcc aag aag gcc ttc ccc tgc tca gtc atc 690
Val Ile Val Lys Val Thr Ser Lys Lys Ala Phe Pro Cys Ser Val Ile

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tcc atc cag gat gtc ctg tgc cct gtc tat gat ctg gac aac agt gta 738
Ser Ile Gln Asp Val Leu Cys Pro Val Tyr Asp Leu Asp Asn Ser Val

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Ala Phe Ile Gly Met Tyr Gln Thr Met Thr Lys Lys Ala Ala Ile Thr

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Val Gln Arg Lys Asp Phe Pro Ser Asn Ser Phe Tyr Val Val Val Val

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gtg aag act gag gac cag gcc tgc gga ggg tcc ttg ccc ttc tac cct 882

Val Lys Thr Glu Asp Gln Ala Cys Gly Gly Ser Leu Pro Phe Tyr Pro

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Phe Val Glu Asp Glu Pro Val Asp Gln Gly His Arg Gln Lys Thr Leu

265

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tca gtg ctg gtc tct cag gct gtc aca tct gag gcc tat gtt ggt ggg 978

Ser Val Leu Val Ser Gln Ala Val Thr Ser Glu Ala Tyr Val Gly Gly

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Met Leu Phe Cys Leu Gly Ile Phe Leu Ser Phe Tyr Leu Leu Thr Val

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Leu Leu Ala Cys Trp Glu Asn Trp Arg Gln Arg Lys Lys Thr Leu Leu

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gtg gcc ata gac cga gcc tgc cca gaa agt ggt cac gct cgg gtc ttg 1122

Val Ala Ile Asp Arg Ala Cys Pro Glu Ser Gly His Ala Arg Val Leu

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335

340

gct gat tca ttt cct ggc agt gcc cct tac gag ggt tac aac tat ggc 1170

Ala Asp Ser Phe Pro Gly Ser Ala Pro Tyr Glu Gly Tyr Asn Tyr Gly

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tcc ttt gaa aat ggt tcc gga tcc act gac ggg ttg gtt gaa agc gca 1218

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365

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ggt tca ggg gac ctc tcc tac agt tac cag ggg cac gac cag ttc aag 1266

Gly Ser Gly Asp Leu Ser Tyr Ser Tyr Gln Gly His Asp Gln Phe Lys

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cgg cgc ctt ccc tct ggc cag atg cgg cag ctg tgc att gcc atg gac 1314

Arg Arg Leu Pro Ser Gly Gln Met Arg Gln Leu Cys Ile Ala Met Asp

395

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cgc tcc ttt gac gca gtg ggt cct cgg cct cga ctg gac tcc atg agc 1362

Arg Ser Phe Asp Ala Val Gly Pro Arg Pro Arg Leu Asp Ser Met Ser

410

415

420

tcc gtg gaa gag gat gac tac gac acg ctg act gac atc gac tca gac 1410

Ser Val Glu Glu Asp Asp Tyr Asp Thr Leu Thr Asp Ile Asp Ser Asp

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aaa aac gtc att cga acc aag caa tac ctc tgt gtg gct gat ctg gca 1458

Lys Asn Val Ile Arg Thr Lys Gln Tyr Leu Cys Val Ala Asp Leu Ala

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cga aag gac aaa cgt gtt ttg cgg aaa aag tac cag att tac ttc tgg 1506

Arg Lys Asp Lys Arg Val Leu Arg Lys Lys Tyr Gln Ile Tyr Phe Trp

460

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aac ata gcc acc att gcg gtc ttc tac gca ctt cct gtg gtg cag ctg 1554

639/735

585 590 595 600

acc tcc ttc atg tac atg att gct ggc ctc tgc atg ctg aag ctc tac 1938

Thr Ser Phe Met Tyr Met Ile Ala Gly Leu Cys Met Leu Lys Leu Tyr

 605 610 615

cag aag cgg cac cca gat atc aac gcc agt gcc tac agt gca tat gcc 1986

Gln Lys Arg His Pro Asp Ile Asn Ala Ser Ala Tyr Ser Ala Tyr Ala

 620 625 630

tgc ttg gcc atc gtc atc ttc ttc tcc gtt ctg ggc gtg gtg ttt ggc 2034

Cys Leu Ala Ile Val Ile Phe Phe Ser Val Leu Gly Val Val Phe Gly

 635 640 645

aaa ggg aac acg gcc ttc tgg att gtc ttc tcc gtc att cac atc atc 2082

Lys Gly Asn Thr Ala Phe Trp Ile Val Phe Ser Val Ile His Ile Ile

 650 655 660

tcc acc ctg ctc ctc agc act cag ctc tat tac atg ggc cgc tgg aag 2130

Ser Thr Leu Leu Leu Ser Thr Gln Leu Tyr Tyr Met Gly Arg Trp Lys

665 670 675 680

ctg gac ttc ggg atc ttc cgc cgc atc ctc cat gtg ctc tac aca gac 2178

Leu Asp Phe Gly Ile Phe Arg Arg Ile Leu His Val Leu Tyr Thr Asp

 685 690 695

tgc atc cgg cag tgc agc ggg ccc ctt tac acg gac cgc atg gtg ctt 2226

Cys Ile Arg Gln Cys Ser Gly Pro Leu Tyr Thr Asp Arg Met Val Leu

 700 705 710

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ctg gtc atg ggc aac att atc aac tgg tgc ctg gct gca tac gga etc 2274
Leu Val Met Gly Asn Ile Ile Asn Trp Ser Leu Ala Ala Tyr Gly Leu
715 720 725

atc atg cgc ccc aat gac ttt gct tcc tac ttg ctg gca att ggc atc 2322
Ile Met Arg Pro Asn Asp Phe Ala Ser Tyr Leu Leu Ala Ile Gly Ile
730 735 740

tgc aac ctg ctg ctt tat ttc gcc ttc tac atc atc atg aag etc cgg 2370
Cys Asn Leu Leu Leu Tyr Phe Ala Phe Tyr Ile Ile Met Lys Leu Arg
745 750 755 760

agc ggc gag agg atc aag etc atc cct ctg ctt tgc atc gtc tgc acc 2418
Ser Gly Glu Arg Ile Lys Leu Ile Pro Leu Leu Cys Ile Val Cys Thr
765 770 775

tcc gtg gtc tgg ggc ttc gcg etc ttc ttc ttc ttc cag gga ctg agc 2466
Ser Val Val Trp Gly Phe Ala Leu Phe Phe Phe Phe Gln Gly Leu Ser
780 785 790

acg tgg cag aaa acc ccc gca gag tcc agg gag cac aac cgc gac tgc 2514
Thr Trp Gln Lys Thr Pro Ala Glu Ser Arg Glu His Asn Arg Asp Cys
795 800 805

atc etc etc gac ttc ttt gat gac cac gat atc tgg cac ttc ctg tcc 2562
Ile Leu Leu Asp Phe Phe Asp Asp His Asp Ile Trp His Phe Leu Ser
810 815 820

tcc att gcc atg ttt ggg tcc ttc ctg gtt ttg ctg acg ttg gat gac 2610

Ser Ile Ala Met Phe Gly Ser Phe Leu Val Leu Leu Thr Leu Asp Asp

825 830 835 840

gac ttg gac aca gta cag cgg gac aag atc tat gtc ttc tagcagcatc 2659

Asp Leu Asp Thr Val Gln Arg Asp Lys Ile Tyr Val Phe

845 850

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acaagaacac cacgggtgtg agtcccagct ctgctgccca gcattggatg tcgtggcaag 2779

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gttgccctctg cggaggagga ggctgctcc gcattcccca gacactggcc aaattgctgc 2899

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Ala Glu Phe Glu Arg Thr Tyr Ala Asp Asp Val Asn Ser Glu Leu Val
35 40 45

Asn Ile Tyr Thr Phe Asn His Thr Val Thr Arg Asn Arg Thr Glu Gly
50 55 60

Val Arg Val Ser Val Asn Val Leu Asn Lys Gln Lys Gly Ala Pro Leu
65 70 75 80

Leu Phe Val Val Arg Gln Lys Glu Ala Val Val Ser Phe Gln Val Pro
85 90 95

Leu Ile Leu Arg Gly Leu Tyr Gln Arg Lys Tyr Leu Tyr Gln Lys Val
100 105 110

Glu Arg Thr Leu Cys Gln Pro Pro Thr Lys Asn Glu Ser Glu Ile Gln
115 120 125

Phe Phe Tyr Val Asp Val Ser Thr Leu Ser Pro Val Asn Thr Thr Tyr
130 135 140

Gln Leu Arg Val Asn Arg Val Asp Asn Phe Val Leu Arg Thr Gly Glu
145 150 155 160

Leu Phe Thr Phe Asn Thr Thr Ala Ala Gln Pro Gln Tyr Phe Lys Tyr
165 170 175

Glu Phe Pro Asp Gly Val Asp Ser Val Ile Val Lys Val Thr Ser Lys
180 185 190

Lys Ala Phe Pro Cys Ser Val Ile Ser Ile Gln Asp Val Leu Cys Pro
195 200 205

Val Tyr Asp Leu Asp Asn Ser Val Ala Phe Ile Gly Met Tyr Gln Thr
210 215 220

Met Thr Lys Lys Ala Ala Ile Thr Val Gln Arg Lys Asp Phe Pro Ser
225 230 235 240

Asn Ser Phe Tyr Val Val Val Val Val Lys Thr Glu Asp Gln Ala Cys
245 250 255

Gly Gly Ser Leu Pro Phe Tyr Pro Phe Val Glu Asp Glu Pro Val Asp
260 265 270

Gln Gly His Arg Gln Lys Thr Leu Ser Val Leu Val Ser Gln Ala Val
275 280 285

Thr Ser Glu Ala Tyr Val Gly Gly Met Leu Phe Cys Leu Gly Ile Phe
646/735

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290

295

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Leu Ser Phe Tyr Leu Leu Thr Val Leu Leu Ala Cys Trp Glu Asn Trp

305

310

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Arg Gln Arg Lys Lys Thr Leu Leu Val Ala Ile Asp Arg Ala Cys Pro

325

330

335

Glu Ser Gly His Ala Arg Val Leu Ala Asp Ser Phe Pro Gly Ser Ala

340

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350

Pro Tyr Glu Gly Tyr Asn Tyr Gly Ser Phe Glu Asn Gly Ser Gly Ser

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360

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Thr Asp Gly Leu Val Glu Ser Ala Gly Ser Gly Asp Leu Ser Tyr Ser

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Tyr Gln Gly His Asp Gln Phe Lys Arg Arg Leu Pro Ser Gly Gln Met

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Arg Gln Leu Cys Ile Ala Met Asp Arg Ser Phe Asp Ala Val Gly Pro

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Arg Pro Arg Leu Asp Ser Met Ser Ser Val Glu Glu Asp Asp Tyr Asp

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Thr Leu Thr Asp Ile Asp Ser Asp Lys Asn Val Ile Arg Thr Lys Gln

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Tyr Leu Cys Val Ala Asp Leu Ala Arg Lys Asp Lys Arg Val Leu Arg

450 455 460

Lys Lys Tyr Gln Ile Tyr Phe Trp Asn Ile Ala Thr Ile Ala Val Phe

465 470 475 480

Tyr Ala Leu Pro Val Val Gln Leu Val Ile Thr Tyr Gln Thr Val Val

485 490 495

Asn Val Thr Gly Asn Gln Asp Ile Cys Tyr Tyr Asn Phe Leu Cys Ala

500 505 510

His Pro Leu Gly Asn Leu Ser Ala Phe Asn Asn Ile Leu Ser Asn Leu

515 520 525

Gly Tyr Ile Leu Leu Gly Leu Leu Phe Leu Leu Ile Ile Leu Gln Arg

530 535 540

Glu Ile Asn His Asn Arg Ala Leu Leu Arg Asn Asp Leu Tyr Ala Leu

545 550 555 560

Glu Cys Gly Ile Pro Lys His Phe Gly Leu Phe Tyr Ala Met Gly Thr

565 570 575

Ala Leu Met Met Glu Gly Leu Leu Ser Ala Cys Tyr His Val Cys Pro

580 585 590

Asn Tyr Thr Asn Phe Gln Phe Asp Thr Ser Phe Met Tyr Met Ile Ala

595 600 605

Gly Leu Cys Met Leu Lys Leu Tyr Gln Lys Arg His Pro Asp Ile Asn

610

615

620

Ala Ser Ala Tyr Ser Ala Tyr Ala Cys Leu Ala Ile Val Ile Phe Phe

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635

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Ser Val Leu Gly Val Val Phe Gly Lys Gly Asn Thr Ala Phe Trp Ile

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650

655

Val Phe Ser Val Ile His Ile Ile Ser Thr Leu Leu Leu Ser Thr Gln

660

665

670

Leu Tyr Tyr Met Gly Arg Trp Lys Leu Asp Phe Gly Ile Phe Arg Arg

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680

685

Ile Leu His Val Leu Tyr Thr Asp Cys Ile Arg Gln Cys Ser Gly Pro

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Leu Tyr Thr Asp Arg Met Val Leu Leu Val Met Gly Asn Ile Ile Asn

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Trp Ser Leu Ala Ala Tyr Gly Leu Ile Met Arg Pro Asn Asp Phe Ala

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Ser Tyr Leu Leu Ala Ile Gly Ile Cys Asn Leu Leu Leu Tyr Phe Ala

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649/735

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Met Phe Ala Leu Gly Leu Pro Phe Leu Val

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Leu Leu Val Ala Ser Val Glu Ser His Leu Gly Val Leu Gly Pro Lys

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Asn Val Ser Gln Lys Asp Ala Glu Phe Glu Arg Thr Tyr Val Asp Glu

30

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gtc aac agc gag ctg gtc aac atc tac acc ttc aac cat act gtg acc 257

Val Asn Ser Glu Leu Val Asn Ile Tyr Thr Phe Asn His Thr Val Thr

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cgc aac agg aca gag ggc gtg cgt gtg tct gtg aac gtc ctg aac aag 305

Arg Asn Arg Thr Glu Gly Val Arg Val Ser Val Asn Val Leu Asn Lys

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Gln Lys Gly Ala Pro Leu Leu Phe Val Val Arg Gln Lys Glu Ala Val

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80

85

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gtg tcc ttc cag gtg ccc cta atc ctg cga ggg atg ttt cag cgc aag 401

Val Ser Phe Gln Val Pro Leu Ile Leu Arg Gly Met Phe Gln Arg Lys

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Tyr Leu Tyr Gln Lys Val Glu Arg Thr Leu Cys Gln Pro Pro Thr Lys

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115

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aat gag tcg gag att cag ttc ttc tac gtg gat gtg tcc acc ctg tca 497

Asn Glu Ser Glu Ile Gln Phe Phe Tyr Val Asp Val Ser Thr Leu Ser

125

130

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cca gtc aac acc aca tac cag ctc cgg gtc agc cgc atg gac gat ttt 545

Pro Val Asn Thr Thr Tyr Gln Leu Arg Val Ser Arg Met Asp Asp Phe

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Val Leu Arg Thr Gly Glu Gln Phe Ser Phe Asn Thr Thr Ala Ala Gln

155

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Pro Gln Tyr Phe Lys Tyr Glu Phe Pro Glu Gly Val Asp Ser Val Ile

175

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652/735

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Ile Gly Met Tyr Gln Thr Met Thr Lys Lys Ala Ala Ile Thr Val Gln

220 225 230

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Arg Lys Asp Phe Pro Ser Asn Ser Phe Tyr Val Val Val Val Val Lys

235 240 245 250

acc gaa gac caa gcc tgc ggg ggc tcc ctg cct ttc tac ccc ttc gca 881

Thr Glu Asp Gln Ala Cys Gly Gly Ser Leu Pro Phe Tyr Pro Phe Ala

255 260 265

gaa gat gaa ccg gtc gat caa ggg cac cgc cag aaa acc ctg tca gtg 929

Glu Asp Glu Pro Val Asp Gln Gly His Arg Gln Lys Thr Leu Ser Val

270 275 280

ctg gtg tct caa gca gtc acg tct gag gca tac gtc agt ggg atg ctc 977

Leu Val Ser Gln Ala Val Thr Ser Glu Ala Tyr Val Ser Gly Met Leu

285 290 295

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Phe Cys Leu Gly Ile Phe Leu Ser Phe Tyr Leu Leu Thr Val Leu Leu

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Ala Cys Trp Glu Asn Trp Arg Gln Lys Lys Lys Thr Leu Leu Val Ala

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| Ser Phe Pro Gly Ser Ser Pro Tyr Glu Gly Tyr Asn Tyr Gly Ser Phe | | | |

| | | | |
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| Glu Asn Val Ser Gly Ser Thr Asp Gly Leu Val Asp Ser Ala Gly Thr | | | |

365 370 375

ggg gac ctc tct tac ggt tac cag ggg cac gac cag ttc aag egg cgc 1265

Gly Asp Leu Ser Tyr Gly Tyr Gln Gly His Asp Gln Phe Lys Arg Arg

380 385 390

ctc ccc tct ggc cag atg cgg cag ctg tgc att gcc atg ggc cgc tcc 1313
Leu Pro Ser Gly Gln Met Arg Gln Leu Cys Ile Ala Met Gly Arg Ser

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| 395 | 400 | 405 | 410 | |
| ttt gaa cct gta ggt act cgg ccc cga gtg gac tcc atg agc tct gtg 1361
Phe Glu Pro Val Gly Thr Arg Pro Arg Val Asp Ser Met Ser Ser Val | | | | |

gag gag gat gac tac gac aca ttg acc gac atc gat tcc gac aag aat . 1409
Glu Glu Asp Asp Tyr Asp Thr Leu Thr Asp Ile Asp Ser Asp Lys Asn

654/735

gtc att cgc acc aag caa tac ctc tat gtg gct gac ctg gca cgg aag 1457
 Val Ile Arg Thr Lys Gln Tyr Leu Tyr Val Ala Asp Leu Ala Arg Lys
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gac aag cgt gtt ctg cgg aaa aag tac cag atc tac ttc tgg aac att 1505
 Asp Lys Arg Val Leu Arg Lys Lys Tyr Gln Ile Tyr Phe Trp Asn Ile
 460 465 470

gcc acc att gct gtc ttc tat gcc ctt cct gtg gtg cag ctg gtg atc 1553
 Ala Thr Ile Ala Val Phe Tyr Ala Leu Pro Val Val Gln Leu Val Ile
 475 480 485 490

acc tac cag acg gtg gtg aat gtc aca ggg aat cag gac atc tgc tac 1601
 Thr Tyr Gln Thr Val Val Asn Val Thr Gly Asn Gln Asp Ile Cys Tyr
 495 500 505

tac aac ttc ctc tgc gcc cac cca ctg ggc aat ctc agc gcc ttc aac 1649
 Tyr Asn Phe Leu Cys Ala His Pro Leu Gly Asn Leu Ser Ala Phe Asn
 510 515 520

aac atc ctc agc aac ctg ggg tac atc ctg ctg ggg ctg ctt ttc ctg 1697
 Asn Ile Leu Ser Asn Leu Gly Tyr Ile Leu Leu Gly Leu Leu Phe Leu
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ctc atc atc ctg caa cgg gag atc aac cac aac cgg gcc ctg ctg cgc 1745
 Leu Ile Ile Leu Gln Arg Glu Ile Asn His Asn Arg Ala Leu Leu Arg
 540 545 550

aat gac ctc tgt gcc ctg gaa tgt ggg atc ccc aaa cac ttt ggg ctt 1793

Asn Asp Leu Cys Ala Leu Glu Cys Gly Ile Pro Lys His Phe Gly Leu

555 560 565 570

ttc tac gcc atg ggc aca gcc ctg atg atg gag ggg ctg ctc agt gct 1841

Phe Tyr Ala Met Gly Thr Ala Leu Met Met Glu Gly Leu Leu Ser Ala

575 580 585

tgc tat cat gtg tgc ccc aac tat acc aat ttc cag ttt gac aca tcg 1889

Cys Tyr His Val Cys Pro Asn Tyr Thr Asn Phe Gln Phe Asp Thr Ser

590 595 600

ttc atg tac atg atc gcc gga ctc tgc atg ctg aag ctc tac cag aag 1937

Phe Met Tyr Met Ile Ala Gly Leu Cys Met Leu Lys Leu Tyr Gln Lys

605 610 615

cgg cac ccg gac atc aac gcc agc gcc tac agt gcc tac gcc tgc ctg 1985

Arg His Pro Asp Ile Asn Ala Ser Ala Tyr Ser Ala Tyr Ala Cys Leu

620 625 630

gcc att gtc atc ttc ttc tct gtg ctg ggc gtg gtc ttt ggc aaa ggg 2033

Ala Ile Val Ile Phe Phe Ser Val Leu Gly Val Val Phe Gly Lys Gly

635 640 645 650

aac acg gcg ttc tgg atc gtc ttc tcc atc att cac atc atc gcc acc 2081

Asn Thr Ala Phe Trp Ile Val Phe Ser Ile Ile His Ile Ile Ala Thr

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ctg ctc ctc agc acg cag ctc tat tac atg ggc cgg tgg aaa ctg gac 2129

Leu Leu Leu Ser Thr Gln Leu Tyr Tyr Met Gly Arg Trp Lys Leu Asp

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tcg ggg atc ttc cgc cgc atc ctc cac gtg ctc tac aca gac tgc atc 2177

Ser Gly Ile Phe Arg Arg Ile Leu His Val Leu Tyr Thr Asp Cys Ile

685

690

695

cgg cag tgc agc ggg ccg ctc tac gtg gac cgc atg gtg ctg ctg gtc 2225

Arg Gln Cys Ser Gly Pro Leu Tyr Val Asp Arg Met Val Leu Leu Val

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atg ggc aac gtc atc aac tgg tgc ctg gct gcc tat ggg ctt atc atg 2273

Met Gly Asn Val Ile Asn Trp Ser Leu Ala Ala Tyr Gly Leu Ile Met

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cgc ccc aat gat ttc gct tcc tac ttg ttg gcc att ggc atc tgc aac 2321

Arg Pro Asn Asp Phe Ala Ser Tyr Leu Leu Ala Ile Gly Ile Cys Asn

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ctg ctc ctt tac ttc gcc ttc tac atc atc atg aag ctc cgg agt ggg 2369

Leu Leu Leu Tyr Phe Ala Phe Tyr Ile Ile Met Lys Leu Arg Ser Gly

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gag agg atc aag ctc atc ccc ctg ctc tgc atc gtt tgc acc tcc gtg 2417

Glu Arg Ile Lys Leu Ile Pro Leu Leu Cys Ile Val Cys Thr Ser Val

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gtc tgg ggc ttc gcg ctc ttc ttc ttc ttc cag gga ctc agc acc tgg 2465

Val Trp Gly Phe Ala Leu Phe Phe Phe Phe Gln Gly Leu Ser Thr Trp

657/735

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| 780 | 785 | 790 | |
| cag aaa acc cct gca gag tcg agg gag cac aac cgg gac tgc atc ctc | | | 2513 |
| Gln Lys Thr Pro Ala Glu Ser Arg Glu His Asn Arg Asp Cys Ile Leu | | | |
| 795 | 800 | 805 | 810 |
| etc gac ttc ttt gac gac cac gac atc tgg cac ttc ctc tcc tcc atc | | | 2561 |
| Leu Asp Phe Phe Asp Asp His Asp Ile Trp His Phe Leu Ser Ser Ile | | | |
| | 815 | 820 | 825 |
| gcc atg ttc ggg tcc ttc ctg gta agc ggg cct ccc ggc cga gcc ggg | | | 2609 |
| Ala Met Phe Gly Ser Phe Leu Val Ser Gly Pro Pro Gly Arg Ala Gly | | | |
| | 830 | 835 | 840 |
| tgg gta cgt gaa ggt agc agc tgc ctc ctt ccc tgt ggc tgatctggcg | | | 2658 |
| Trp Val Arg Glu Gly Ser Ser Cys Leu Leu Pro Cys Gly | | | |
| | 845 | 850 | 855 |
| tccacacccc aggtgttgct gacactggat gacgacctgg atacttagaa aggggcttca | | | 2718 |
| ggaagggatg tgctgtttcc ctctacgtgc ccagtcctag cctcgctcta ggaccaggg | | | 2778 |
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<212> PRT

<213> Homo sapiens

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Glu Ser His Leu Gly Val Leu Gly Pro Lys Asn Val Ser Gln Lys Asp

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Ala Glu Phe Glu Arg Thr Tyr Val Asp Glu Val Asn Ser Glu Leu Val

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40

45

Asn Ile Tyr Thr Phe Asn His Thr Val Thr Arg Asn Arg Thr Glu Gly

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55

60

Val Arg Val Ser Val Asn Val Leu Asn Lys Gln Lys Gly Ala Pro Leu

65

70

75

80

Leu Phe Val Val Arg Gln Lys Glu Ala Val Val Ser Phe Gln Val Pro

85

90

95

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Leu Ile Leu Arg Gly Met Phe Gln Arg Lys Tyr Leu Tyr Gln Lys Val
100 105 110

Glu Arg Thr Leu Cys Gln Pro Pro Thr Lys Asn Glu Ser Glu Ile Gln
115 120 125

Phe Phe Tyr Val Asp Val Ser Thr Leu Ser Pro Val Asn Thr Thr Tyr
130 135 140

Gln Leu Arg Val Ser Arg Met Asp Asp Phe Val Leu Arg Thr Gly Glu
145 150 155 160

Gln Phe Ser Phe Asn Thr Thr Ala Ala Gln Pro Gln Tyr Phe Lys Tyr
165 170 175

Glu Phe Pro Glu Gly Val Asp Ser Val Ile Val Lys Val Thr Ser Asn
180 185 190

Lys Ala Phe Pro Cys Ser Val Ile Ser Ile Gln Asp Val Leu Cys Pro
195 200 205

Val Tyr Asp Leu Asp Asn Asn Val Ala Phe Ile Gly Met Tyr Gln Thr
210 215 220

Met Thr Lys Lys Ala Ala Ile Thr Val Gln Arg Lys Asp Phe Pro Ser
225 230 235 240

Asn Ser Phe Tyr Val Val Val Val Val Lys Thr Glu Asp Gln Ala Cys
660/735

245

250

255

Gly Gly Ser Leu Pro Phe Tyr Pro Phe Ala Glu Asp Glu Pro Val Asp

260

265

270

Gln Gly His Arg Gln Lys Thr Leu Ser Val Leu Val Ser Gln Ala Val

275

280

285

Thr Ser Glu Ala Tyr Val Ser Gly Met Leu Phe Cys Leu Gly Ile Phe

290

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300

Leu Ser Phe Tyr Leu Leu Thr Val Leu Leu Ala Cys Trp Glu Asn Trp

305

310

315

320

Arg Gln Lys Lys Lys Thr Leu Leu Val Ala Ile Asp Arg Ala Cys Pro

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330

335

Glu Ser Gly His Pro Arg Val Leu Ala Asp Ser Phe Pro Gly Ser Ser

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345

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Pro Tyr Glu Gly Tyr Asn Tyr Gly Ser Phe Glu Asn Val Ser Gly Ser

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360

365

Thr Asp Gly Leu Val Asp Ser Ala Gly Thr Gly Asp Leu Ser Tyr Gly

370

375

380

Tyr Gln Gly His Asp Gln Phe Lys Arg Arg Leu Pro Ser Gly Gln Met

385

390

395

400

Arg Gln Leu Cys Ile Ala Met Gly Arg Ser Phe Glu Pro Val Gly Thr

405

410

415

Arg Pro Arg Val Asp Ser Met Ser Ser Val Glu Glu Asp Asp Tyr Asp

420

425

430

Thr Leu Thr Asp Ile Asp Ser Asp Lys Asn Val Ile Arg Thr Lys Gln

435

440

445

Tyr Leu Tyr Val Ala Asp Leu Ala Arg Lys Asp Lys Arg Val Leu Arg

450

455

460

Lys Lys Tyr Gln Ile Tyr Phe Trp Asn Ile Ala Thr Ile Ala Val Phe

465

470

475

480

Tyr Ala Leu Pro Val Val Gln Leu Val Ile Thr Tyr Gln Thr Val Val

485

490

495

Asn Val Thr Gly Asn Gln Asp Ile Cys Tyr Tyr Asn Phe Leu Cys Ala

500

505

510

His Pro Leu Gly Asn Leu Ser Ala Phe Asn Asn Ile Leu Ser Asn Leu

515

520

525

Gly Tyr Ile Leu Leu Gly Leu Leu Phe Leu Leu Ile Ile Leu Gln Arg

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535

540

Glu Ile Asn His Asn Arg Ala Leu Leu Arg Asn Asp Leu Cys Ala Leu

545

550

555

560

Glu Cys Gly Ile Pro Lys His Phe Gly Leu Phe Tyr Ala Met Gly Thr
565 570 575

Ala Leu Met Met Glu Gly Leu Leu Ser Ala Cys Tyr His Val Cys Pro
580 585 590

Asn Tyr Thr Asn Phe Gln Phe Asp Thr Ser Phe Met Tyr Met Ile Ala
595 600 605

Gly Leu Cys Met Leu Lys Leu Tyr Gln Lys Arg His Pro Asp Ile Asn
610 615 620

Ala Ser Ala Tyr Ser Ala Tyr Ala Cys Leu Ala Ile Val Ile Phe Phe
625 630 635 640

Ser Val Leu Gly Val Val Phe Gly Lys Gly Asn Thr Ala Phe Trp Ile
645 650 655

Val Phe Ser Ile Ile His Ile Ile Ala Thr Leu Leu Leu Ser Thr Gln
660 665 670

Leu Tyr Tyr Met Gly Arg Trp Lys Leu Asp Ser Gly Ile Phe Arg Arg
675 680 685

Ile Leu His Val Leu Tyr Thr Asp Cys Ile Arg Gln Cys Ser Gly Pro
690 695 700

Leu Tyr Val Asp Arg Met Val Leu Leu Val Met Gly Asn Val Ile Asn
663/735

705 710 715 720

Trp Ser Leu Ala Ala Tyr Gly Leu Ile Met Arg Pro Asn Asp Phe Ala
725 730 735

Ser Tyr Leu Leu Ala Ile Gly Ile Cys Asn Leu Leu Leu Tyr Phe Ala
740 745 750

Phe Tyr Ile Ile Met Lys Leu Arg Ser Gly Glu Arg Ile Lys Leu Ile
755 760 765

Pro Leu Leu Cys Ile Val Cys Thr Ser Val Val Trp Gly Phe Ala Leu
770 775 780

Phe Phe Phe Phe Gln Gly Leu Ser Thr Trp Gln Lys Thr Pro Ala Glu
785 790 795 800

Ser Arg Glu His Asn Arg Asp Cys Ile Leu Leu Asp Phe Phe Asp Asp
805 810 815

His Asp Ile Trp His Phe Leu Ser Ser Ile Ala Met Phe Gly Ser Phe
820 825 830

Leu Val Ser Gly Pro Pro Gly Arg Ala Gly Trp Val Arg Glu Gly Ser
835 840 845

Ser Cys Leu Leu Pro Cys Gly
850 855

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Met

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Glu Cys Thr Glu Ala Lys Lys His Cys Trp Tyr Phe Glu Gly Leu Tyr

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25

30

Pro Thr Tyr Tyr Ile Cys Arg Ser Tyr Glu Asp Cys Cys Gly Ser Arg

35

40

45

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Cys Cys Val Arg Ala Leu Ser Ile Gln Arg Leu Trp Tyr Phe Trp Phe

50 55 60 65

ctt ctg atg atg ggc gtg ctt ttc tgc tgc gga gcc ggc ttc ttc atc 298

Leu Leu Met Met Gly Val Leu Phe Cys Cys Gly Ala Gly Phe Phe Ile

70 75 80

cgg agg cgc atg tac ccc ccg ccg ctg atc gag gag cca gcc ttc aat 346

Arg Arg Arg Met Tyr Pro Pro Pro Leu Ile Glu Glu Pro Ala Phe Asn

85 90 95

gtg tcc tac acc agg cag ccc cca aat ccc ggc cca gga gcc cag cag 394

Val Ser Tyr Thr Arg Gln Pro Pro Asn Pro Gly Pro Gly Ala Gln Gln

100 105 110

ccg ggg ccg ccc tat tac acc gac cca gga gga ccg ggg atg aac cct 442

Pro Gly Pro Pro Tyr Tyr Thr Asp Pro Gly Gly Pro Gly Met Asn Pro

115 120 125

gtc ggg aat tcc atg gca atg gct ttc cag gtc cca ccc aac tca ccc 490

Val Gly Asn Ser Met Ala Met Ala Phe Gln Val Pro Pro Asn Ser Pro

130 135 140 145

cag ggg agt gtg gcc tgc ccg ccc cct cca gcc tac tgc aac acg cct 538

Gln Gly Ser Val Ala Cys Pro Pro Pro Pro Ala Tyr Cys Asn Thr Pro

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Pro Pro Pro Tyr Glu Gln Val Val Lys Ala Lys

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170

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- <211> 172
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Arg Cys Cys Val Arg Ala Leu Ser Ile Gln Arg Leu Trp Tyr Phe Trp

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Phe Leu Leu Met Met Gly Val Leu Phe Cys Cys Gly Ala Gly Phe Phe

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75

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Ile Arg Arg Arg Met Tyr Pro Pro Pro Leu Ile Glu Glu Pro Ala Phe

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Asn Val Ser Tyr Thr Arg Gln Pro Pro Asn Pro Gly Pro Gly Ala Gln

100

105

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Gln Pro Gly Pro Pro Tyr Tyr Thr Asp Pro Gly Gly Pro Gly Met Asn

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Pro Val Gly Asn Ser Met Ala Met Ala Phe Gln Val Pro Pro Asn Ser

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Pro Gln Gly Ser Val Ala Cys Pro Pro Pro Pro Ala Tyr Cys Asn Thr

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Pro Pro Pro Pro Tyr Glu Gln Val Val Lys Ala Lys

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acc tgc aca ctc tca ggg aac cgg gac acc ctc tgg cat ctc ttc aat 315

Thr Cys Thr Leu Ser Gly Asn Arg Asp Thr Leu Trp His Leu Phe Asn

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acc ctt cag cgg cgg ccc ggc tgg gtg gag tac ttc att gcg gca ctg 363

Thr Leu Gln Arg Arg Pro Gly Trp Val Glu Tyr Phe Ile Ala Ala Leu

65 70 75

agg ggc tgt gag cta gtt gat ctc gcg gac gaa gtg gcc tct gtc tac 411

Arg Gly Cys Glu Leu Val Asp Leu Ala Asp Glu Val Ala Ser Val Tyr

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cag agc tac cag cct cgg acc tcg gac cgt ccc cca gac cca ctg gag 459

Gln Ser Tyr Gln Pro Arg Thr Ser Asp Arg Pro Pro Asp Pro Leu Glu

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Pro Pro Ser Leu Pro Ala Glu Arg Pro Gly Pro Pro Thr Pro Ala Ala

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gcc cac agc atc ccc tac aac agc tgc aga gag aag gag cca agt tac 555

Ala His Ser Ile Pro Tyr Asn Ser Cys Arg Glu Lys Glu Pro Ser Tyr

125 130 135 140

ccc atg cct gtc cag gag acc cag gcg cca gag tcc cca gga gag aat 603

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Gly Lys Gln Gly Ala Glu Ser Asp Gln Ala Glu Pro Ile Ile Cys Ser

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Ser Gly Ala Glu Ala Pro Ala Asn Ser Leu Pro Ser Lys Val Pro Thr

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acc ttg atg cct gtg aac aca gtg gcc ctg aaa gtg cct gcc aac cca 1083

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gca tct gtc agc aca gtg ccc tcc aag ttg cca act agc tca aag ccc 1131

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cct ggt gca gtg cct tct aat gcg ctc acc aat cca gca cca tcc aaa 1179

Pro Gly Ala Val Pro Ser Asn Ala Leu Thr Asn Pro Ala Pro Ser Lys

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ttg ccc atc aac tca acc cgt gct ggc atg gtg cca tcc aaa gtg cct 1227

Leu Pro Ile Asn Ser Thr Arg Ala Gly Met Val Pro Ser Lys Val Pro

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act agc atg gtg ctc acc aag gtg tct gcc agc aca gtc ccc act gac 1275

Thr Ser Met Val Leu Thr Lys Val Ser Ala Ser Thr Val Pro Thr Asp

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ggg agc agc aga aat gag gag acc cca gca gct cca aca ccc gcc ggc 1323

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gcc act gga ggc agc tca gcc tgg cta gac agc agc tct gag aat agg 1371

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ggc ctt ggg tcg gag ctg agt aag cct ggc gtg ctg gca tcc cag gta 1419

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gac agc ccg ttc tcg ggc tgc ttc gag gat ctt gcc atc agt gcc agc 1467

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acc tcc ttg ggc atg ggg ccc tgc cat ggc cca gag gag aat gag tat 1515

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aag tcc gag ggc acc ttt ggg atc cac gtg gct gag aac ccc agc atc 1563

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cag ctc ctg gag ggc aac cct ggg cca cct gcg gac ccg gat ggc ggc 1611

Gln Leu Leu Glu Gly Asn Pro Gly Pro Pro Ala Asp Pro Asp Gly Gly

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ccc agg cca caa gcc gac cgg aag ttc cag gag agg gag gtg cca tgc 1659

Pro Arg Pro Gln Ala Asp Arg Lys Phe Gln Glu Arg Glu Val Pro Cys

495

500

505

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1. 2010年12月31日，甲企业“应收账款”科目所属各明细科目的借方余额如下：A公司100000元，B公司200000元，C公司300000元，D公司400000元。2011年1月1日，甲企业“坏账准备”科目贷方余额为100000元。2011年1月15日，甲企业得知C公司破产，应收C公司账款300000元有80%无法收回。2011年2月1日，甲企业得知D公司因火灾将厂房烧毁，应收D公司账款400000元有90%无法收回。2011年3月1日，甲企业得知B公司因火灾将厂房烧毁，应收B公司账款200000元有80%无法收回。2011年3月31日，甲企业根据期末应收账款明细账余额，计提坏账准备。

510 515 520

Val Leu Val Val Thr Leu Leu Val Val Leu Tyr Arg Arg Arg Leu His

525 530 535 540

[REDACTED]

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Ala Glu Ser Asp Gln Ala Glu Pro Ile Ile Cys Ser Ser Gly Ala Glu

275

280

285

Ala Pro Ala Asn Ser Leu Pro Ser Lys Val Pro Thr Thr Leu Met Pro

290

295

300

Val Asn Thr Val Ala Leu Lys Val Pro Ala Asn Pro Ala Ser Val Ser

305

310

315

320

Thr Val Pro Ser Lys Leu Pro Thr Ser Ser Lys Pro Pro Gly Ala Val

325

330

335

Pro Ser Asn Ala Leu Thr Asn Pro Ala Pro Ser Lys Leu Pro Ile Asn

340

345

350

Ser Thr Arg Ala Gly Met Val Pro Ser Lys Val Pro Thr Ser Met Val

355

360

365

Leu Thr Lys Val Ser Ala Ser Thr Val Pro Thr Asp Gly Ser Ser Arg

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Asn Glu Glu Thr Pro Ala Ala Pro Thr Pro Ala Gly Ala Thr Gly Gly

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395

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Ser Ser Ala Trp Leu Asp Ser Ser Ser Glu Asn Arg Gly Leu Gly Ser

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Glu Leu Ser Lys Pro Gly Val Leu Ala Ser Gln Val Asp Ser Pro Phe

420

425

430

Ser Gly Cys Phe Glu Asp Leu Ala Ile Ser Ala Ser Thr Ser Leu Gly

435

440

445

Met Gly Pro Cys His Gly Pro Glu Glu Asn Glu Tyr Lys Ser Glu Gly

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455

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Thr Phe Gly Ile His Val Ala Glu Asn Pro Ser Ile Gln Leu Leu Glu

465

470

475

480

Gly Asn Pro Gly Pro Pro Ala Asp Pro Asp Gly Gly Pro Arg Pro Gln

485

490

495

Ala Asp Arg Lys Phe Gln Glu Arg Glu Val Pro Cys His Arg Pro Ser

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Pro Gly Ala Leu Trp Leu Gln Val Ala Val Thr Gly Val Leu Val Val

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gcggggcgcc gacgaggagt gcaggactca ggaaggcgca gtgcgcggcg acagagcccc 180

gggaaggagg cagggaagg ccgggcttgg gggcaggtgg tccgggcac cagccttgaa 240

g atg cac aag agg aaa gga ccc ccg gga ccc ccg ggc aga ggc gcc gcg 289

Met His Lys Arg Lys Gly Pro Pro Gly Pro Pro Gly Arg Gly Ala Ala

1 5 10 15

gcc gcc cgc cag ctg ggc ctg ctg gtt gac ctc tcc cca gat ggc ctg 337

Ala Ala Arg Gln Leu Gly Leu Leu Val Asp Leu Ser Pro Asp Gly Leu

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atg atc cct gag gac ggg gct aac gat gaa gaa ctg gag gct gag ttc 385

Met Ile Pro Glu Asp Gly Ala Asn Asp Glu Glu Leu Glu Ala Glu Phe

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ttg gct ttg gtc ggg ggc cag ccc cca gcc ctg gag aag ctc aaa ggc 433

Leu Ala Leu Val Gly Gly Gln Pro Pro Ala Leu Glu Lys Leu Lys Gly

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aaa ggt ccc ttg ccg atg gag gcc att gag aag atg gcc agc ctg tgc 481

Lys Gly Pro Leu Pro Met Glu Ala Ile Glu Lys Met Ala Ser Leu Cys

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atg aga gac ccg gat gag gat gag gag gag ggg acg gat gag gac gac 529

Met Arg Asp Pro Asp Glu Asp Glu Glu Glu Gly Thr Asp Glu Asp Asp

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ttg gag gct gat gat gac ctg ctg gcg gag cta aat gag gtc ctt gga 577

Leu Glu Ala Asp Asp Asp Leu Leu Ala Glu Leu Asn Glu Val Leu Gly

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gag gag cag aag gct tca gag acc cca cct cct gtg gcc cag ccg aag 625

Glu Glu Gln Lys Ala Ser Glu Thr Pro Pro Pro Val Ala Gln Pro Lys

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cct gag gcc cct cat ccg ggg ctg gag acc acc ttg cag gag agg ctg 673

Pro Glu Ala Pro His Pro Gly Leu Glu Thr Thr Leu Gln Glu Arg Leu

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Ala Leu Tyr Gln Thr Ala Ile Glu Ser Ala Arg Gln Ala Gly Asp Ser

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gcc aag atg cgg cgc tac gat cgg ggg ctt aaa aca ctg gaa aac ctg 769

Ala Lys Met Arg Arg Tyr Asp Arg Gly Leu Lys Thr Leu Glu Asn Leu

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ctc gcc tcc atc cgt aag ggc aat gcc att gac gaa gcg gac atc ccg 817

Leu Ala Ser Ile Arg Lys Gly Asn Ala Ile Asp Glu Ala Asp Ile Pro

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ccg cca gtg gcc ata gga aaa ggc ccg gcg tcc acg cct acc tac agc 865

Pro Pro Val Ala Ile Gly Lys Gly Pro Ala Ser Thr Pro Thr Tyr Ser

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cct gca ccc acc cag ccg gcc cct aga atc gcg tca gcc cca gag ccc 913

Pro Ala Pro Thr Gln Pro Ala Pro Arg Ile Ala Ser Ala Pro Glu Pro

210

215

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agg gtc acc ctg gag gga cct tct gcc acc gcc cca gcc tca tct cca 961

Arg Val Thr Leu Glu Gly Pro Ser Ala Thr Ala Pro Ala Ser Ser Pro

225

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ggc ttg gct aag ccc cag atg ccc cca ggt ccc tgc agc cct ggc cct 1009

Gly Leu Ala Lys Pro Gln Met Pro Pro Gly Pro Cys Ser Pro Gly Pro

245

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ctg gcc cag ttg cag agc cgc cag cgc gac tac aag ctg gct gcc ctc 1057

Leu Ala Gln Leu Gln Ser Arg Gln Arg Asp Tyr Lys Leu Ala Ala Leu

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265

270

cac gcc aag cag cag gga gat acc act gct gcc gct aga cac ttc cgc 1105

His Ala Lys Gln Gln Gly Asp Thr Thr Ala Ala Ala Arg His Phe Arg

275

280

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gtg gct aag agc ttt gat gct gtc ttg gag gcc ctg agc cgg ggt gag 1153

Val Ala Lys Ser Phe Asp Ala Val Leu Glu Ala Leu Ser Arg Gly Glu

290

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ccc gtg gac ctc tcc tgc ctg ccc cct cca ccc gac cag ctg ccc cca 1201

Pro Val Asp Leu Ser Cys Leu Pro Pro Pro Pro Asp Gln Leu Pro Pro

305

310

315

320

gac cca ccg tca cca ccg tcg cag cct ccg acc ccc gct acg gcg ccc 1249

Asp Pro Pro Ser Pro Pro Ser Gln Pro Pro Thr Pro Ala Thr Ala Pro

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tcc aca aca gag gtg ccc cca ccc ccg agg acc ctg ctg gag gcg ctg 1297

Ser Thr Thr Glu Val Pro Pro Pro Pro Arg Thr Leu Leu Glu Ala Leu

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gag cag cgg atg gag cgg tac cag gtg gcc gca gcc cag gcc aag agc 1345

Glu Gln Arg Met Glu Arg Tyr Gln Val Ala Ala Ala Gln Ala Lys Ser

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aag ggg gac cag cgg aaa gct cga atg cac gag cgc atc gtc aag caa 1393

Lys Gly Asp Gln Arg Lys Ala Arg Met His Glu Arg Ile Val Lys Gln

370

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tac caa gat gcc atc cga gcc cac aag gct ggc cga gcc gtg gat gtc 1441

Tyr Gln Asp Ala Ile Arg Ala His Lys Ala Gly Arg Ala Val Asp Val

385 390 395 400

gct gaa ttg ccc gtg ccc cca ggc ttc ccc cca atc cag ggc ctg gag 1489
Ala Glu Leu Pro Val Pro Pro Gly Phe Pro Pro Ile Gln Gly Leu Glu
405 410 415

gcc acc aag ccc acc cag cag agt ctg gtg ggt gtc ctg gag act gcc 1537
Ala Thr Lys Pro Thr Gln Gln Ser Leu Val Gly Val Leu Glu Thr Ala
420 425 430

atg aag ctg gcc aac cag gat gaa ggc cca gag gat gaa gag gat gag 1585
Met Lys Leu Ala Asn Gln Asp Glu Gly Pro Glu Asp Glu Glu Asp Glu
435 440 445

gtg cct aag aag cag aac agc cct gtg gcc ccc aca gcc cag ccc aaa 1633
Val Pro Lys Lys Gln Asn Ser Pro Val Ala Pro Thr Ala Gln Pro Lys
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gcc cca ccc tca aga act ccc cag tcg gga tca gcc cca aca gcc aaa 1681
Ala Pro Pro Ser Arg Thr Pro Gln Ser Gly Ser Ala Pro Thr Ala Lys
465 470 475 480

gcg ccc ccc aaa gcc aca tcc acc aga gcc cag cag cag ctg gcc ttc 1729
Ala Pro Pro Lys Ala Thr Ser Thr Arg Ala Gln Gln Gln Leu Ala Phe
485 490 495

cta gag ggc cgc aag aag cag ctc ctg cag gcc gca ctg cga gcc aag 1777
Leu Glu Gly Arg Lys Lys Gln Leu Leu Gln Ala Ala Leu Arg Ala Lys
500 505 510

686/735

cag aaa aac gac gtg gag ggt gcc aag atg cac ctg cgc caa gcc aag 1825

Gln Lys Asn Asp Val Glu Gly Ala Lys Met His Leu Arg Gln Ala Lys

515

520

525

gga ctg gag cct atg ctg gag gcc tcg cgc aat ggg ctg cct gtg gac 1873

Gly Leu Glu Pro Met Leu Glu Ala Ser Arg Asn Gly Leu Pro Val Asp

530

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atc acc aag gtg ccg cct gcc cct gtc aac aag gac gac ttt gcc ctg 1921

Ile Thr Lys Val Pro Pro Ala Pro Val Asn Lys Asp Asp Phe Ala Leu

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gtc cag cgg cct ggc ccg ggt ctg tct cag gag gcc gcc cgg cgc tat 1969

Val Gln Arg Pro Gly Pro Gly Leu Ser Gln Glu Ala Ala Arg Arg Tyr

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ggt gaa ctc acc aag ctc ata cgg cag cag cac gag atg tgc ctg aac 2017

Gly Glu Leu Thr Lys Leu Ile Arg Gln Gln His Glu Met Cys Leu Asn

580

585

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cac tca aac caa ttc acc cag ctg ggc aac atc act gaa acc acc aag 2065

His Ser Asn Gln Phe Thr Gln Leu Gly Asn Ile Thr Glu Thr Thr Lys

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ttt gaa aag ttg gcg gag gac tgt aag cgg agc atg gac att ctg aag 2113

Phe Glu Lys Leu Ala Glu Asp Cys Lys Arg Ser Met Asp Ile Leu Lys

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caa gcc ttc gtc cgg ggt ctc ccc acg ccc acc gcc cgc ttt gag caa 2161

Gln Ala Phe Val Arg Gly Leu Pro Thr Pro Thr Ala Arg Phe Glu Gln

625 630 635 640

agg acc ttc agc gtc atc aag atc ttc cct gac ctc agc agc aac gac 2209

Arg Thr Phe Ser Val Ile Lys Ile Phe Pro Asp Leu Ser Ser Asn Asp

645 650 655

atg ctc ctc ttc atc gtg aag ggc atc aac ttg ccc aca ccc cca gga 2257

Met Leu Leu Phe Ile Val Lys Gly Ile Asn Leu Pro Thr Pro Pro Gly

660 665 670

ctg tcc cct ggc gat ctg gat gtc ttt gtt cgg ttt gac ttc ccc tat 2305

Leu Ser Pro Gly Asp Leu Asp Val Phe Val Arg Phe Asp Phe Pro Tyr

675 680 685

ccc aac gtg gaa gaa gct cag aaa gac aag acc agt gtg atc aag aac 2353

Pro Asn Val Glu Glu Ala Gln Lys Asp Lys Thr Ser Val Ile Lys Asn

690 695 700

aca gac tcc cct gag ttc aag gag cag ttc aaa ctc tgc atc aac cgc 2401

Thr Asp Ser Pro Glu Phe Lys Glu Gln Phe Lys Leu Cys Ile Asn Arg

705 710 715 720

agc cac cgt ggc ttc cga agg gcc atc cag acc aag ggc atc aag ttc 2449

Ser His Arg Gly Phe Arg Arg Ala Ile Gln Thr Lys Gly Ile Lys Phe

725 730 735

gaa gtg gtt cac aag ggg ggg ctg ttc aag act gac cgg gtg ctg ggg 2497

Glu Val Val His Lys Gly Gly Leu Phe Lys Thr Asp Arg Val Leu Gly

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aca gcc cag ctg aag ctg gat gca ctg gag ata gca tgt gag gtc cgg 2545

Thr Ala Gln Leu Lys Leu Asp Ala Leu Glu Ile Ala Cys Glu Val Arg

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gag atc ctt gag gtc ctg gat ggt cgc cgg ccc aca ggg ggg cga ctg 2593

Glu Ile Leu Glu Val Leu Asp Gly Arg Arg Pro Thr Gly Gly Arg Leu

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gag gta atg gtc cgg att cgg gag cca ctg aca gcc cag cag ttg gag 2641

Glu Val Met Val Arg Ile Arg Glu Pro Leu Thr Ala Gln Gln Leu Glu

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790

795

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acg acg aca gag agg tgg ctg gtc att gac cct gtg ccg gca gct gtg 2689

Thr Thr Thr Glu Arg Trp Leu Val Ile Asp Pro Val Pro Ala Ala Val

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810

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ccc aca cag gtt gct ggg ccc aaa ggg aag gcc cct cct gtg cct gcc 2737

Pro Thr Gln Val Ala Gly Pro Lys Gly Lys Ala Pro Pro Val Pro Ala

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cct gca agg gag tca ggg aac aga tca gcc cgg ccc ctg cat agc ctc 2785

Pro Ala Arg Glu Ser Gly Asn Arg Ser Ala Arg Pro Leu His Ser Leu

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845

agt gtg ctg gcg ttt gac caa gag cgt ctg gag cgg aag atc ctg gcc 2833

Ser Val Leu Ala Phe Asp Gln Glu Arg Leu Glu Arg Lys Ile Leu Ala

689/735

850

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ctc agg cag gcg cgg cgg ccg gtg ccc cca gaa gtg gcc cag cag tac 2881

Leu Arg Gln Ala Arg Arg Pro Val Pro Pro Glu Val Ala Gln Gln Tyr

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875

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cag gac atc atg caa cgc agc cag tgg cag agg gca cag ctg gag cag 2929

Gln Asp Ile Met Gln Arg Ser Gln Trp Gln Arg Ala Gln Leu Glu Gln

885

890

895

ggg ggt gtg ggc atc cga cgg gaa tac aca gcc cag ctg gag cgg cag 2977

Gly Gly Val Gly Ile Arg Arg Glu Tyr Thr Ala Gln Leu Glu Arg Gln

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905

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ctg cag ttc tac acg gag gct gcc cgg cgc ctg ggc aac gat ggc agc 3025

Leu Gln Phe Tyr Thr Glu Ala Ala Arg Arg Leu Gly Asn Asp Gly Ser

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agg gat gct gca aag gag gcg ctc tat agg cgg aat ctg gta ggg agt 3073

Arg Asp Ala Ala Lys Glu Ala Leu Tyr Arg Arg Asn Leu Val Gly Ser

930

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gag ctg cag cgg ctc cgc agg tgaggagccc atggggcggg cagccccag 3124

Glu Leu Gln Arg Leu Arg Arg

945

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<213> Homo sapiens

<400> 172

Met His Lys Arg Lys Gly Pro Pro Gly Pro Pro Gly Arg Gly Ala Ala

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Ala Ala Arg Gln Leu Gly Leu Leu Val Asp Leu Ser Pro Asp Gly Leu

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Met Ile Pro Glu Asp Gly Ala Asn Asp Glu Glu Leu Glu Ala Glu Phe

35 40 45

Leu Ala Leu Val Gly Gly Gln Pro Pro Ala Leu Glu Lys Leu Lys Gly
 50 55 60

Lys Gly Pro Leu Pro Met Glu Ala Ile Glu Lys Met Ala Ser Leu Cys
 65 70 75 80

Met Arg Asp Pro Asp Glu Asp Glu Glu Glu Gly Thr Asp Glu Asp Asp
 85 90 95

Leu Glu Ala Asp Asp Asp Leu Leu Ala Glu Leu Asn Glu Val Leu Gly
 100 105 110

Glu Glu Gln Lys Ala Ser Glu Thr Pro Pro Pro Val Ala Gln Pro Lys
 115 120 125

Pro Glu Ala Pro His Pro Gly Leu Glu Thr Thr Leu Gln Glu Arg Leu
 130 135 140

Ala Leu Tyr Gln Thr Ala Ile Glu Ser Ala Arg Gln Ala Gly Asp Ser
 145 150 155 160

Ala Lys Met Arg Arg Tyr Asp Arg Gly Leu Lys Thr Leu Glu Asn Leu
 165 170 175

Leu Ala Ser Ile Arg Lys Gly Asn Ala Ile Asp Glu Ala Asp Ile Pro
 180 185 190

Pro Pro Val Ala Ile Gly Lys Gly Pro Ala Ser Thr Pro Thr Tyr Ser
 195 200 205

Pro Ala Pro Thr Gln Pro Ala Pro Arg Ile Ala Ser Ala Pro Glu Pro

210

215

220

Arg Val Thr Leu Glu Gly Pro Ser Ala Thr Ala Pro Ala Ser Ser Pro

225

230

235

240

Gly Leu Ala Lys Pro Gln Met Pro Pro Gly Pro Cys Ser Pro Gly Pro

245

250

255

Leu Ala Gln Leu Gln Ser Arg Gln Arg Asp Tyr Lys Leu Ala Ala Leu

260

265

270

His Ala Lys Gln Gln Gly Asp Thr Thr Ala Ala Ala Arg His Phe Arg

275

280

285

Val Ala Lys Ser Phe Asp Ala Val Leu Glu Ala Leu Ser Arg Gly Glu

290

295

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Pro Val Asp Leu Ser Cys Leu Pro Pro Pro Pro Asp Gln Leu Pro Pro

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Asp Pro Pro Ser Pro Pro Ser Gln Pro Pro Thr Pro Ala Thr Ala Pro

325

330

335

Ser Thr Thr Glu Val Pro Pro Pro Pro Arg Thr Leu Leu Glu Ala Leu

340

345

350

Glu Gln Arg Met Glu Arg Tyr Gln Val Ala Ala Ala Gln Ala Lys Ser

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Gln Lys Asn Asp Val Glu Gly Ala Lys Met His Leu Arg Gln Ala Lys

515

520

525

Gly Leu Glu Pro Met Leu Glu Ala Ser Arg Asn Gly Leu Pro Val Asp

530

535

540

Ile Thr Lys Val Pro Pro Ala Pro Val Asn Lys Asp Asp Phe Ala Leu

545

550

555

560

Val Gln Arg Pro Gly Pro Gly Leu Ser Gln Glu Ala Ala Arg Arg Tyr

565

570

575

Gly Glu Leu Thr Lys Leu Ile Arg Gln Gln His Glu Met Cys Leu Asn

580

585

590

His Ser Asn Gln Phe Thr Gln Leu Gly Asn Ile Thr Glu Thr Thr Lys

595

600

605

Phe Glu Lys Leu Ala Glu Asp Cys Lys Arg Ser Met Asp Ile Leu Lys

610

615

620

Gln Ala Phe Val Arg Gly Leu Pro Thr Pro Thr Ala Arg Phe Glu Gln

625

630

635

640

Arg Thr Phe Ser Val Ile Lys Ile Phe Pro Asp Leu Ser Ser Asn Asp

645

650

655

Met Leu Leu Phe Ile Val Lys Gly Ile Asn Leu Pro Thr Pro Pro Gly

660

665

670

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Leu Ser Pro Gly Asp Leu Asp Val Phe Val Arg Phe Asp Phe Pro Tyr
675 680 685

Pro Asn Val Glu Glu Ala Gln Lys Asp Lys Thr Ser Val Ile Lys Asn
690 695 700

Thr Asp Ser Pro Glu Phe Lys Glu Gln Phe Lys Leu Cys Ile Asn Arg
705 710 715 720

Ser His Arg Gly Phe Arg Arg Ala Ile Gln Thr Lys Gly Ile Lys Phe
725 730 735

Glu Val Val His Lys Gly Gly Leu Phe Lys Thr Asp Arg Val Leu Gly
740 745 750

Thr Ala Gln Leu Lys Leu Asp Ala Leu Glu Ile Ala Cys Glu Val Arg
755 760 765

Glu Ile Leu Glu Val Leu Asp Gly Arg Arg Pro Thr Gly Gly Arg Leu
770 775 780

Glu Val Met Val Arg Ile Arg Glu Pro Leu Thr Ala Gln Gln Leu Glu
785 790 795 800

Thr Thr Thr Glu Arg Trp Leu Val Ile Asp Pro Val Pro Ala Ala Val
805 810 815

Pro Thr Gln Val Ala Gly Pro Lys Gly Lys Ala Pro Pro Val Pro Ala
696/735

830

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gcacctagca ggctctctgg gaaaaaaaaa tcc atg ggt gac aga aga ttt att 594

Met Gly Asp Arg Arg Phe Ile

698/735

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aat gca act gcc aat aat act tgc att gtt gat gat tcc ttc aag tat 690
Asn Ala Thr Ala Asn Asn Thr Cys Ile Val Asp Asp Ser Phe Lys Tyr
25 30 35

aat ttg aat ggt gct gtc tat agt gtt gta ttc atc ctg ggt cta ata 738
Asn Leu Asn Gly Ala Val Tyr Ser Val Val Phe Ile Leu Gly Leu Ile
40 45 50 55

acc aac agt gcc tcc ctg ttt gtc ttc tgc ttc cgc atg aaa atg aga 786
Thr Asn Ser Ala Ser Leu Phe Val Phe Cys Phe Arg Met Lys Met Arg
60 65 70

agt gag acg gct act ttc atc acc aac ctg gcc ctc tct gat ttg ctt 834
Ser Glu Thr Ala Thr Phe Ile Thr Asn Leu Ala Leu Ser Asp Leu Leu
75 80 85

ttt gtt tgt acc cta cct ttc aaa ata ttt tac aac ttt aat cgc cac 882
Phe Val Cys Thr Leu Pro Phe Lys Ile Phe Tyr Asn Phe Asn Arg His
90 95 100

tgg cct ttt ggt gac acc ctc tgt aag atc tca ggg act gcg ttc ctc 930
Trp Pro Phe Gly Asp Thr Leu Cys Lys Ile Ser Gly Thr Ala Phe Leu
105 110 115

acc aac atc tat ggg agc atg ctc ttc ctc acc tgc atc agt gtg gat 978

Thr Asn Ile Tyr Gly Ser Met Leu Phe Leu Thr Cys Ile Ser Val Asp

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135

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Arg Phe Leu Ala Ile Val Tyr Pro Phe Arg Ser Arg Thr Ile Arg Thr

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agg agg aat tcc gcc att gtg tgc gct gga gtc tgg atc cta gtc ctc 1074

Arg Arg Asn Ser Ala Ile Val Cys Ala Gly Val Trp Ile Leu Val Leu

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Ser Gly Gly Ile Ser Ala Ser Leu Phe Ser Thr Thr Asn Val Asn Asn

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gcg acc acc act tgc ttt gaa ggc ttc tcc aaa cgt gtc tgg aag aca 1170

Ala Thr Thr Thr Cys Phe Glu Gly Phe Ser Lys Arg Val Trp Lys Thr

185

190

195

tac ctg tcc aag atc act ata ttc att gaa gtt gtt gga ttc atc att 1218

Tyr Leu Ser Lys Ile Thr Ile Phe Ile Glu Val Val Gly Phe Ile Ile

200

205

210

215

cct ctg ata ttg aat gtt tct tgt tct tct gtg gtg ctt aga acc ctc 1266

Pro Leu Ile Leu Asn Val Ser Cys Ser Ser Val Val Leu Arg Thr Leu

220

225

230

cgc aag cct gca aca ttg tct cag att ggg acc aat aag aaa aaa gtg 1314

Arg Lys Pro Ala Thr Leu Ser Gln Ile Gly Thr Asn Lys Lys Lys Val

235

240

245

ttg aag atg atc aca gtg cat atg gca gtg ttt gtg gta tgc ttt gta 1362

Leu Lys Met Ile Thr Val His Met Ala Val Phe Val Val Cys Phe Val

250

255

260

cca tac aac tcc gtt ctc ttt tta tat gcc ttg gta cgc tcc caa gcc 1410

Pro Tyr Asn Ser Val Leu Phe Leu Tyr Ala Leu Val Arg Ser Gln Ala

265

270

275

att act aat tgc tta ttg gaa agg ttt gca aag atc atg tac cca att 1458

Ile Thr Asn Cys Leu Leu Glu Arg Phe Ala Lys Ile Met Tyr Pro Ile

280

285

290

295

acc ttg tgc ctt gca act ctg aat tgt tgc ttt gat cct ttt atc tat 1506

Thr Leu Cys Leu Ala Thr Leu Asn Cys Cys Phe Asp Pro Phe Ile Tyr

300

305

310

tac ttc act ctt gaa tcc ttt cag aag tcc ttt tat atc aat aca cat 1554

Tyr Phe Thr Leu Glu Ser Phe Gln Lys Ser Phe Tyr Ile Asn Thr His

315

320

325

ata agg atg gag tgc ctg ttt aag act gag aca cct ctg acc ccc aaa 1602

Ile Arg Met Glu Ser Leu Phe Lys Thr Glu Thr Pro Leu Thr Pro Lys

330

335

340

cct tcc ctt cca gct atc caa gag gaa gtt agt gat caa aca aca aat 1650

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DATE 01-03-2001 BY 60322 UCBAW

350

355

Asn Gly Gly Glu Leu Met Leu Glu Ser Thr Phe

365

370

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attagtgtca gcttttaaaa ctttcttttt aaaataattc tagaattttc atatgaaatt 2363

gttaatcctg aaaggtgcta cttatgtgcc tggcaggtat aaaatggaaa actcataaaa 2423

ttaacagtgt caatttataa aaaaaaaaaac tttaagcaac actatattat ttcttaagat 2483

tttcatttat cctttatggg ggtggggatt ggcttgtaga aaatatttat tcttcatgtt 2543

aaatgttggg gacacattac agccagagag ctacagtatt tgtgcccagg tcaggagtaa 2603

attgaaaaag taagtgaata gaatagtagc agcaagatat cttagagctt atattagtag 2663

ttttaaggt ggtgggtaga tagctgtaat tttgaaatcc atactctctt ctgtacattt 2723

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aagatgtgta cat 2796

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<212> PRT

<213> Mus musculus

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Met Gly Asp Arg Arg Phe Ile Asp Phe Gln Phe Gln Asp Leu Asn Ser

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Ser Leu Arg Pro Arg Leu Gly Asn Ala Thr Ala Asn Asn Thr Cys Ile

20 25 30

Val Asp Asp Ser Phe Lys Tyr Asn Leu Asn Gly Ala Val Tyr Ser Val
35 40 45

Val Phe Ile Leu Gly Leu Ile Thr Asn Ser Ala Ser Leu Phe Val Phe
50 55 60

Cys Phe Arg Met Lys Met Arg Ser Glu Thr Ala Thr Phe Ile Thr Asn
65 70 75 80

Leu Ala Leu Ser Asp Leu Leu Phe Val Cys Thr Leu Pro Phe Lys Ile
85 90 95

Phe Tyr Asn Phe Asn Arg His Trp Pro Phe Gly Asp Thr Leu Cys Lys
100 105 110

Ile Ser Gly Thr Ala Phe Leu Thr Asn Ile Tyr Gly Ser Met Leu Phe
115 120 125

Leu Thr Cys Ile Ser Val Asp Arg Phe Leu Ala Ile Val Tyr Pro Phe
130 135 140

Arg Ser Arg Thr Ile Arg Thr Arg Arg Asn Ser Ala Ile Val Cys Ala
145 150 155 160

Gly Val Trp Ile Leu Val Leu Ser Gly Gly Ile Ser Ala Ser Leu Phe
165 170 175

Ser Thr Thr Asn Val Asn Asn Ala Thr Thr Thr Cys Phe Glu Gly Phe
180 185 190

Ser Lys Arg Val Trp Lys Thr Tyr Leu Ser Lys Ile Thr Ile Phe Ile
195 200 205

Glu Val Val Gly Phe Ile Ile Pro Leu Ile Leu Asn Val Ser Cys Ser
210 215 220

Ser Val Val Leu Arg Thr Leu Arg Lys Pro Ala Thr Leu Ser Gln Ile
225 230 235 240

Gly Thr Asn Lys Lys Lys Val Leu Lys Met Ile Thr Val His Met Ala
245 250 255

Val Phe Val Val Cys Phe Val Pro Tyr Asn Ser Val Leu Phe Leu Tyr
260 265 270

Ala Leu Val Arg Ser Gln Ala Ile Thr Asn Cys Leu Leu Glu Arg Phe
275 280 285

Ala Lys Ile Met Tyr Pro Ile Thr Leu Cys Leu Ala Thr Leu Asn Cys
290 295 300

Cys Phe Asp Pro Phe Ile Tyr Tyr Phe Thr Leu Glu Ser Phe Gln Lys
305 310 315 320

Ser Phe Tyr Ile Asn Thr His Ile Arg Met Glu Ser Leu Phe Lys Thr
325 330 335

Glu Thr Pro Leu Thr Pro Lys Pro Ser Leu Pro Ala Ile Gln Glu Glu
705/735

tgc att gtt gat gat tcc ttc aag tat aat ctc aat ggt gct gtc tac 204
 Cys Ile Val Asp Asp Ser Phe Lys Tyr Asn Leu Asn Gly Ala Val Tyr
 35 40 45

agt gtt gta ttc atc ttg ggt ctg ata acc aac agt gtc tct ctg ttt 252
 Ser Val Val Phe Ile Leu Gly Leu Ile Thr Asn Ser Val Ser Leu Phe
 50 55 60

gtc ttc tgt ttc cgc atg aaa atg aga agt gag act gct att ttt atc 300
 Val Phe Cys Phe Arg Met Lys Met Arg Ser Glu Thr Ala Ile Phe Ile
 65 70 75

acc aat cta gct gtc tct gat ttg ctt ttt gtc tgt aca cta cct ttt 348
 Thr Asn Leu Ala Val Ser Asp Leu Leu Phe Val Cys Thr Leu Pro Phe
 80 85 90

aaa ata ttt tac aac ttc aac cgc cac tgg cct ttt ggt gac acc ctc 396
 Lys Ile Phe Tyr Asn Phe Asn Arg His Trp Pro Phe Gly Asp Thr Leu
 95 100 105 110

tgc aag atc tct gga act gca ttc ctt acc aac atc tat ggg agc atg 444
 Cys Lys Ile Ser Gly Thr Ala Phe Leu Thr Asn Ile Tyr Gly Ser Met
 115 120 125

ctc ttt ctc acc tgt att agt gtg gat cgt ttc ctg gcc att gtc tat 492
 Leu Phe Leu Thr Cys Ile Ser Val Asp Arg Phe Leu Ala Ile Val Tyr
 130 135 140

255 260 265 270

ttg tat gcc ctg gtg cgc tcc caa gct att act aat tgc ttt ttg gaa 924

Leu Tyr Ala Leu Val Arg Ser Gln Ala Ile Thr Asn Cys Phe Leu Glu

275 280 285

aga ttt gca aag atc atg tac cca atc acc ttg tgc ctt gca act ctg 972

Arg Phe Ala Lys Ile Met Tyr Pro Ile Thr Leu Cys Leu Ala Thr Leu

290 295 300

aac tgt tgt ttt gac cct ttc atc tat tac ttc acc ctt gaa tcc ttt 1020

Asn Cys Cys Phe Asp Pro Phe Ile Tyr Tyr Phe Thr Leu Glu Ser Phe

305 310 315

cag aag tcc ttc tac atc aat gcc cac atc aga atg gag tcc ctg ttt 1068

Gln Lys Ser Phe Tyr Ile Asn Ala His Ile Arg Met Glu Ser Leu Phe

320 325 330

aag act gaa aca cct ttg acc aca aag cct tcc ctt cca gct att caa 1116

Lys Thr Glu Thr Pro Leu Thr Thr Lys Pro Ser Leu Pro Ala Ile Gln

335 340 345 350

gag gaa gtg agt gat caa aca aca aat aat ggt ggt gaa tta atg cta 1164

Glu Glu Val Ser Asp Gln Thr Thr Asn Asn Gly Gly Glu Leu Met Leu

355 360 365

gaa tcc acc ttt taggtatgag aaatgtgttc aggtccagat atggttttctc 1216

Glu Ser Thr Phe

ctataatfff tcctatgcta taaactaaag atttgaagct aatgatactg agaataatgc 1276

accaaateca gtcagataca ttgttttgaa ggtatactgt agagttttta ttgctgtttt 1336

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gcttggttgg aatttcattg tatgcatta tccaggtggc tagtggcatt tgataatata 1456

gagatgactt tgaaacttte aaaaaggtat ttctattcca atgatatttg gtaattaggt 1516

tgggcctata aatatagaac aaattcaggg atttttaaaa aattgtgtta ctactgatat 1576

atgctagttt tattttattt ttttgactg tcattgagtt tatttttagca caagaatatt 1636

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tgtgcatttt gaaaacagaa aacaaattgc gttggcatgt acgtgggtgg gaagaaaaag 1756

aaaattaaca ggattttacac aattataatc accagcagtg tgagtttaaa aaacttcgtt 1816

gtttttacac caaattaaaa ttttcatgtc aaacttcaaa gccagaaaagc tgctaaatac 1876

gtgtctggca ggtaaaagct ggaaaattac ttaaaacagg aaagtgtaa taaaaaaact 1936

tgagcaacac caacatattt ttctttaaaa tgtcacgtta tcttcatttt gggaactag 1996

gttctataaa atatttatcc tccctgttat actttggagc acagcacagc cagaaaagggg 2056

ctgcatttgt gccaggtca ggagcaaatt gaaaaaaaa ataaagtaat actaaaaaat 2116

caactataa acccaaaaca tttattaaaa cctgaattaa tccttttttg aggaggagt 2176

agagatatat aacctgaaaa tacttattct ttcttatcga attttggagc ctaatatagc 2236

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cct 2299

<210> 176

<211> 370

<212> PRT

<213> Homo sapiens

<400> 176

Met Gly Asp Arg Arg Phe Ile Asp Phe Gln Phe Gln Asp Ser Asn Ser

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15

Ser Leu Arg Pro Arg Leu Gly Asn Ala Thr Ala Asn Asn Thr Cys Ile

20

25

30

Val Asp Asp Ser Phe Lys Tyr Asn Leu Asn Gly Ala Val Tyr Ser Val

35

40

45

Val Phe Ile Leu Gly Leu Ile Thr Asn Ser Val Ser Leu Phe Val Phe

50

55

60

Cys Phe Arg Met Lys Met Arg Ser Glu Thr Ala Ile Phe Ile Thr Asn
65 70 75 80

Leu Ala Val Ser Asp Leu Leu Phe Val Cys Thr Leu Pro Phe Lys Ile
85 90 95

Phe Tyr Asn Phe Asn Arg His Trp Pro Phe Gly Asp Thr Leu Cys Lys
100 105 110

Ile Ser Gly Thr Ala Phe Leu Thr Asn Ile Tyr Gly Ser Met Leu Phe
115 120 125

Leu Thr Cys Ile Ser Val Asp Arg Phe Leu Ala Ile Val Tyr Pro Phe
130 135 140

Arg Ser Arg Thr Ile Arg Thr Arg Arg Asn Ser Ala Ile Val Cys Ala
145 150 155 160

Gly Val Trp Ile Leu Val Leu Ser Gly Gly Ile Ser Ala Ser Leu Phe
165 170 175

Ser Thr Thr Asn Val Asn Asn Ala Thr Thr Thr Cys Phe Glu Gly Phe
180 185 190

Ser Lys Arg Val Trp Lys Thr Tyr Leu Ser Lys Ile Thr Ile Phe Ile
195 200 205

Glu Val Val Gly Phe Ile Ile Pro Leu Ile Leu Asn Val Ser Cys Ser
712/735

210

215

220

Ser Val Val Leu Arg Thr Leu Arg Lys Pro Ala Thr Leu Ser Gln Ile

225

230

235

240

Gly Thr Asn Lys Lys Lys Val Leu Lys Met Ile Thr Val His Met Ala

245

250

255

Val Phe Val Val Cys Phe Val Pro Tyr Asn Ser Val Leu Phe Leu Tyr

260

265

270

Ala Leu Val Arg Ser Gln Ala Ile Thr Asn Cys Phe Leu Glu Arg Phe

275

280

285

Ala Lys Ile Met Tyr Pro Ile Thr Leu Cys Leu Ala Thr Leu Asn Cys

290

295

300

Cys Phe Asp Pro Phe Ile Tyr Tyr Phe Thr Leu Glu Ser Phe Gln Lys

305

310

315

320

Ser Phe Tyr Ile Asn Ala His Ile Arg Met Glu Ser Leu Phe Lys Thr

325

330

335

Glu Thr Pro Leu Thr Thr Lys Pro Ser Leu Pro Ala Ile Gln Glu Glu

340

345

350

Val Ser Asp Gln Thr Thr Asn Asn Gly Gly Glu Leu Met Leu Glu Ser

355

360

365

Thr Phe
370

<210> 177
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<400> 177

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Met Ala Arg Gly Ser Leu Arg Arg

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Leu Leu Arg Leu Leu Val Leu Gly Leu Trp Leu Ala Leu Leu Arg Ser

10 15 20

gtg gcc ggg gag caa gcg cca ggc acc gcc ccc tgc tcc cgc ggc agc 149
Val Ala Gly Glu Gln Ala Pro Gly Thr Ala Pro Cys Ser Arg Gly Ser

25 30 35 40

tcc tgg agc gcg gac ctg gac aag tgc atg gac tgc gcg tct tgc agg 197
Ser Trp Ser Ala Asp Leu Asp Lys Cys Met Asp Cys Ala Ser Cys Arg

45

50

55

gcg cga ccg cac agc gac ttc tgc ctg ggc tgc gct gca gca cct cct 245

Ala Arg Pro His Ser Asp Phe Cys Leu Gly Cys Ala Ala Ala Pro Pro

60

65

70

gcc ccc ttc cgg ctg ctt tgg ccc atc ctt ggg ggc gct ctg agc ctg 293

Ala Pro Phe Arg Leu Leu Trp Pro Ile Leu Gly Gly Ala Leu Ser Leu

75

80

85

acc ttc gtg ctg ggg ctg ctt tct ggc ttt ttg gtc tgg aga cga tgc 341

Thr Phe Val Leu Gly Leu Leu Ser Gly Phe Leu Val Trp Arg Arg Cys

90

95

100

cgc agg aga gag aag ttc acc acc ccc ata gag gag acc ggc gga gag 389

Arg Arg Arg Glu Lys Phe Thr Thr Pro Ile Glu Glu Thr Gly Gly Glu

105

110

115

120

ggc tgc cca gct gtg gcg ctg atc cag tgacaatgtg cccctgcca 436

Gly Cys Pro Ala Val Ala Leu Ile Gln

125

gccggggctc gccactcat cattcattca tccattctag agccagtctc tgcctcccag 496

acgcggcggg agccaagctc ctccaaccac aaggggggtg gggggcgggtg aatcacctcc 556

gaggcctggg tccagggttc aggggaacct tccaaggtgt ctggttgccc tgcctctggc 616

tccagaacag aaaggagacc tcacgtggc tcacacaaaa cagctgacac tgactaagga 676

actgcagcat ttgcacaggg gaggggggtg ccctccttcc tagaggccct gggggccagg 736

ctgacttggg gggcagactt gacactaggc cccactcact cagatgtcct gaaattccac 796

cacgggggtc accctggggg gttagggacc tatttttaac actagggggc tggcccacta 856

ggagggtgg ccctaagata cagaccccc caactcccca aagcggggag gagatattta 916

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<210> 178

<211> 129

<212> PRT

<213> Homo sapiens

<400> 178

Met Ala Arg Gly Ser Leu Arg Arg Leu Leu Arg Leu Leu Val Leu Gly

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Leu Trp Leu Ala Leu Leu Arg Ser Val Ala Gly Glu Gln Ala Pro Gly

20 25 30

Thr Ala Pro Cys Ser Arg Gly Ser Ser Trp Ser Ala Asp Leu Asp Lys

35 40 45

Cys Met Asp Cys Ala Ser Cys Arg Ala Arg Pro His Ser Asp Phe Cys

50 55 60

Leu Gly Cys Ala Ala Ala Pro Pro Ala Pro Phe Arg Leu Leu Trp Pro
65 70 75 80

Ile Leu Gly Gly Ala Leu Ser Leu Thr Phe Val Leu Gly Leu Leu Ser
85 90 95

Gly Phe Leu Val Trp Arg Arg Cys Arg Arg Arg Glu Lys Phe Thr Thr
100 105 110

Pro Ile Glu Glu Thr Gly Gly Glu Gly Cys Pro Ala Val Ala Leu Ile
115 120 125

Gln

- <210> 179
- <211> 3631
- <212> DNA
- <213> Homo sapiens

- <220>
- <221> CDS
- <222> (191).. (3244)

<400> 179

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ccacctggaa gggaaccgcc ttgttctcac ctgccttgcc gaaggagct ggcctttgga 180

gttcaagtgg atg cgc gat gac agt gag ctc acc acc tac agc agc gaa 229

Met Arg Asp Asp Ser Glu Leu Thr Thr Tyr Ser Ser Glu

1

5

10

tat aag tac att att cca tct ttg cag aag ctc gat gct ggg ttt tac 277

Tyr Lys Tyr Ile Ile Pro Ser Leu Gln Lys Leu Asp Ala Gly Phe Tyr

15

20

25

cgc tgc gtg gtg cga aac aga atg gga gca ctc ctg caa aga aaa tca 325

Arg Cys Val Val Arg Asn Arg Met Gly Ala Leu Leu Gln Arg Lys Ser

30

35

40

45

gaa gtt caa gtc gca tat atg gga agt ttc atg gat acg gac cag agg 373

Glu Val Gln Val Ala Tyr Met Gly Ser Phe Met Asp Thr Asp Gln Arg

50

55

60

aaa aca gtt tct caa gga cgt gca gcg att cta aac ctg ctg ccc atc 421

Lys Thr Val Ser Gln Gly Arg Ala Ala Ile Leu Asn Leu Leu Pro Ile

65

70

75

acc agc tac ccc aga cct caa gtg act tgg ttt aga gaa ggg cac aag 469

Thr Ser Tyr Pro Arg Pro Gln Val Thr Trp Phe Arg Glu Gly His Lys

80

85

90

att att cca agc aac aga ata gcc atc aca ttg gag aat cag ctg gtg 517

Ile Ile Pro Ser Asn Arg Ile Ala Ile Thr Leu Glu Asn Gln Leu Val

95

100

105

atc ctc gcc acc aca acc agt gat gcc ggg gca tac tac gtg cag gcc 565

Ile Leu Ala Thr Thr Thr Ser Asp Ala Gly Ala-Tyr Tyr Val Gln Ala

110

115

120

125

gtg aat gag aaa aat gga gaa aac aag aca agc cca ttc att cat ttg 613

Val Asn Glu Lys Asn Gly Glu Asn Lys Thr Ser Pro Phe Ile His Leu

130

135

140

agc ata gca aga gat gtt ggc aca cct gaa acc atg gcc cca acc att 661

Ser Ile Ala Arg Asp Val Gly Thr Pro Glu Thr Met Ala Pro Thr Ile

145

150

155

gtg gtt ccc ccg ggc aac aga agt gtg gtg gct gga tcc agt gag acc 709

Val Val Pro Pro Gly Asn Arg Ser Val Val Ala Gly Ser Ser Glu Thr

160

165

170

acc ttg gaa tgt ata gcc agt gcc agg cct gtg gag gac ctg agt gtg 757

Thr Leu Glu Cys Ile Ala Ser Ala Arg Pro Val Glu Asp Leu Ser Val

175

180

185

acc tgg aag agg aat gga gtg aga atc acc agt ggc ctc cac agc ttt 805

Thr Trp Lys Arg Asn Gly Val Arg Ile Thr Ser Gly Leu His Ser Phe

190

195

200

205

gga aga cgc ctc acc atc agc aac ccg acg tcc gcg gac acc ggg cca 853

Gly Arg Arg Leu Thr Ile Ser Asn Pro Thr Ser Ala Asp Thr Gly Pro

210

215

220

tac gtc tgc gag gcg gcg ctg ccg ggg agc gct ttt gaa ccg gcc agg 901

Tyr Val Cys Glu Ala Ala Leu Pro Gly Ser Ala Phe Glu Pro Ala Arg

225

230

235

gcg acg gcc ttt ctt ttc atc ata gag cca cca tat ttt act gct gag 949

Ala Thr Ala Phe Leu Phe Ile Ile Glu Pro Pro Tyr Phe Thr Ala Glu

240

245

250

ccc gag agt cgg att tca gct gaa gta gaa gaa act gtg gac atc gga 997

Pro Glu Ser Arg Ile Ser Ala Glu Val Glu Glu Thr Val Asp Ile Gly

255

260

265

tgt caa gcc atg ggg gtc ccc ctt ccc acc ctc cag tgg tac aag gat 1045

Cys Gln Ala Met Gly Val Pro Leu Pro Thr Leu Gln Trp Tyr Lys Asp

270

275

280

285

gcc atc tcc atc agc agg ctc cag aat cct cga tac aaa gtg ctc gcc 1093

Ala Ile Ser Ile Ser Arg Leu Gln Asn Pro Arg Tyr Lys Val Leu Ala

290

295

300

agc gga ggc ctg cgc atc cag aag ctg cgt cca gag gac tcc gga atc 1141

Ser Gly Gly Leu Arg Ile Gln Lys Leu Arg Pro Glu Asp Ser Gly Ile

305

310

315

ttc cag tgc ttc gcc agc aat gaa gga ggg gag atc cag acc cac acc 1189

Phe Gln Cys Phe Ala Ser Asn Glu Gly Gly Glu Ile Gln Thr His Thr

320

325

330

tac ctg gat gta acc aat atc gct cca gtg ttc acc cag cgg cca gtg 1237

Tyr Leu Asp Val Thr Asn Ile Ala Pro Val Phe Thr Gln Arg Pro Val

335

340

345

gac acc aca gtt act gac ggg atg aca gcc att cta agg tgt gag gtg 1285

Asp Thr Thr Val Thr Asp Gly Met Thr Ala Ile Leu Arg Cys Glu Val

350

355

360

365

tcc ggg gct ccc aaa ccc gcc atc acc tgg aaa aga gaa aac cac att 1333

Ser Gly Ala Pro Lys Pro Ala Ile Thr Trp Lys Arg Glu Asn His Ile

370

375

380

ctg gcc agt ggc tct gtc cgg att cct agg ttc atg ctt ctt gaa tcg 1381

Leu Ala Ser Gly Ser Val Arg Ile Pro Arg Phe Met Leu Leu Glu Ser

385

390

395

ggg ggt cta cag atc gcg ccc gtc ttc atc cag gat gcc ggc aac tac 1429

Gly Gly Leu Gln Ile Ala Pro Val Phe Ile Gln Asp Ala Gly Asn Tyr

400

405

410

acc tgc tat gcg gcc aac aca gag ggc tcc ctg aat gca tcg gcc acg 1477

Thr Cys Tyr Ala Ala Asn Thr Glu Gly Ser Leu Asn Ala Ser Ala Thr

415

420

425

ctc act gtg tgg aat cgg acg tcc atc gtc cac cct cct gag gac cac 1525

Leu Thr Val Trp Asn Arg Thr Ser Ile Val His Pro Pro Glu Asp His

430

435

440

445

gtg gtg att aag ggg acc acg gcc acg ctg cac tgt ggt gcc aca cat 1573

Val Val Ile Lys Gly Thr Thr Ala Thr Leu His Cys Gly Ala Thr His

450

455

460

gac ccc cgg gtt tca ctc cgc tac gtt tgg aag aag gac aac gtg gcc 1621

Asp Pro Arg Val Ser Leu Arg Tyr Val Trp Lys Lys Asp Asn Val Ala

465

470

475

ctg act cca tcg agc acg tct agg atc gtg gtg gag aag gac ggg tcc 1669

Leu Thr Pro Ser Ser Thr Ser Arg Ile Val Val Glu Lys Asp Gly Ser

480

485

490

ctt ctc atc agc cag acg tgg tca ggc gac atc ggt gac tac agc tgc 1717

Leu Leu Ile Ser Gln Thr Trp Ser Gly Asp Ile Gly Asp Tyr Ser Cys

495

500

505

gag att gtt tct gaa gga ggg aat gac tcc agg atg gcc cgg ctg gaa 1765

Glu Ile Val Ser Glu Gly Gly Asn Asp Ser Arg Met Ala Arg Leu Glu

510

515

520

525

gtg att gaa ctg cct cat tca cct cag aac ctc ctg gtc agc cct aat 1813

Val Ile Glu Leu Pro His Ser Pro Gln Asn Leu Leu Val Ser Pro Asn

530

535

540

tct tcc cac agc cac gcc gtg gtg ctc tct tgg gtc cgg ccc ttt gat 1861

Ser Ser His Ser His Ala Val Val Leu Ser Trp Val Arg Pro Phe Asp

545

550

555

gga aac agt cct att ctt tat tac atc gtg gag ctg tct gaa aac aac 1909

722/735

Gly Asn Ser Pro Ile Leu Tyr Tyr Ile Val Glu Leu Ser Glu Asn Asn
560 565 570

tct cca tgg aag gtg cat ctg tca aac gtt ggc cct gag atg aca ggc 1957
Ser Pro Trp Lys Val His Leu Ser Asn Val Gly Pro Glu Met Thr Gly
575 580 585

gtc acc gtg agt ggc ctg act ccg gct cgt acc tat caa ttc cgg gtg 2005
Val Thr Val Ser Gly Leu Thr Pro Ala Arg Thr Tyr Gln Phe Arg Val
590 595 600 605

tgc gcg gtg aat gaa gtg ggc agg ggc cag tac agt gcc gag aca agc 2053
Cys Ala Val Asn Glu Val Gly Arg Gly Gln Tyr Ser Ala Glu Thr Ser
610 615 620

agg ttg atg cta cct gaa gaa cca ccc agt gct ccc ccg aaa aat ata 2101
Arg Leu Met Leu Pro Glu Glu Pro Pro Ser Ala Pro Pro Lys Asn Ile
625 630 635

gtg gcc agt ggg cgg act aat cag tcc att atg gtc cag tgg cag cca 2149
Val Ala Ser Gly Arg Thr Asn Gln Ser Ile Met Val Gln Trp Gln Pro
640 645 650

ccc cca gaa aca gag cac aac ggg gtg ttg cgt gga tac atc ctc agg 2197
Pro Pro Glu Thr Glu His Asn Gly Val Leu Arg Gly Tyr Ile Leu Arg
655 660 665

tac cgc ctg gct ggc ctt ccc gga gag tac cag cag cgg aac atc acc 2245
Tyr Arg Leu Ala Gly Leu Pro Gly Glu Tyr Gln Gln Arg Asn Ile Thr
723/735

.. .. .

| | | | | |
|-----------------------------------------------------------------|-----|-----|-----|------|
| 670 | 675 | 680 | 685 | |
| agc ccg gag gtg aac tac tgc ctg gtg aca gac ctg atc atc tgg aca | | | | 2293 |
| Ser Pro Glu Val Asn Tyr Cys Leu Val Thr Asp Leu Ile Ile Trp Thr | | | | |
| | 690 | 695 | 700 | |
| cag tat gag ata cag gtg gcg gcg tac aac ggg gcc ggt ctg ggc gtc | | | | 2341 |
| Gln Tyr Glu Ile Gln Val Ala Ala Tyr Asn Gly Ala Gly Leu Gly Val | | | | |
| | 705 | 710 | 715 | |
| ttc agc agg gca gtg acc gag tac acc ttg cag gga gtg ccc acc gcg | | | | 2389 |
| Phe Ser Arg Ala Val Thr Glu Tyr Thr Leu Gln Gly Val Pro Thr Ala | | | | |
| | 720 | 725 | 730 | |
| ccc ccg cag aac gtg cag acg gaa gcc gtg aac tcc acc acc att cag | | | | 2437 |
| Pro Pro Gln Asn Val Gln Thr Glu Ala Val Asn Ser Thr Thr Ile Gln | | | | |
| | 735 | 740 | 745 | |
| ttc ctg tgg aac cct ccg cct cag cag ttt atc aat ggc atc aac cag | | | | 2485 |
| Phe Leu Trp Asn Pro Pro Pro Gln Gln Phe Ile Asn Gly Ile Asn Gln | | | | |
| 750 | 755 | 760 | 765 | |
| gga tac aag ctt ctg gca tgg ccg gca gat gcc ccc gag gct gtc act | | | | 2533 |
| Gly Tyr Lys Leu Leu Ala Trp Pro Ala Asp Ala Pro Glu Ala Val Thr | | | | |
| | 770 | 775 | 780 | |
| gtg gtc act att gcc cca gat ttc cac gga gtc cac cat gga cac ata | | | | 2581 |
| Val Val Thr Ile Ala Pro Asp Phe His Gly Val His His Gly His Ile | | | | |
| | 785 | 790 | 795 | |
| 724/735 | | | | |

gtg act gcc gtg ggc act ggc ctg gtg act tca tcc acc att tct tct 2965

Val Thr Ala Val Gly Thr Gly Leu Val Thr Ser Ser Thr Ile Ser Ser

910 915 920 925

gga gtg ccc cca gac ctt cct ggt gcc cca tcc aac ctg gtc att tcc 3013

Gly Val Pro Pro Asp Leu Pro Gly Ala Pro Ser Asn Leu Val Ile Ser

930 935 940

aac atc agc cct cgc tcc gcc acc ctt cag ttc cgg cca ggc tat gac 3061

Asn Ile Ser Pro Arg Ser Ala Thr Leu Gln Phe Arg Pro Gly Tyr Asp

945 950 955

ggg aaa acg tcc atc tcc agg tgg att gtt gag ggg cag atg aga cat 3109

Gly Lys Thr Ser Ile Ser Arg Trp Ile Val Glu Gly Gln Met Arg His

960 965 970

caa ggt gtt gga tta cct gcc gag gtc aca cag cca agc cat gaa gcc 3157

Gln Gly Val Gly Leu Pro Ala Glu Val Thr Gln Pro Ser His Glu Ala

975 980 985

gga ttg gag cct gca aac ctc gga agt ctg tgg ctg ctc agc ctg gtg 3205

Gly Leu Glu Pro Ala Asn Leu Gly Ser Leu Trp Leu Leu Ser Leu Val

990 995 1000 1005

tat tgg tgt tac agc cag aaa ctt tgg gaa ttc tct tgt tagttggtta 3254

Tyr Trp Cys Tyr Ser Gln Lys Leu Trp Glu Phe Ser Cys

1010 1015

gttttactgt aattttctat aaagaattca tatcatctgt taatggcgac agtttttggt 3314

tcttcctttg aattttttat attcttttctt tctctttttt gtttcttctt ctttgagtat 3374

tttgtaatct tactgggagg gctaaagegt cttctatcat atcgaattgg gacaatgata 3434

gaagacaatc ttgtttttgt cactctaaag aaattattgt aagattttat catcaggtat 3494

gacatttaca ccattgatgt aggcttttta aaaaatatat ccagcctgta ttgggttaag 3554

atgattcttt tctgatcctg atttcctagg agttggtttt ttttttttta aagcataaat 3614

aaatttaatt gcatcag 3631

<210> 180

<211> 1018

<212> PRT

<213> Homo sapiens

<400> 180

Met Arg Asp Asp Ser Glu Leu Thr Thr Tyr Ser Ser Glu Tyr Lys Tyr

1

5

10

15

Ile Ile Pro Ser Leu Gln Lys Leu Asp Ala Gly Phe Tyr Arg Cys Val

20

25

30

Val Arg Asn Arg Met Gly Ala Leu Leu Gln Arg Lys Ser Glu Val Gln

35

40

45

Val Ala Tyr Met Gly Ser Phe Met Asp Thr Asp Gln Arg Lys Thr Val

50

55

60

Ser Gln Gly Arg Ala Ala Ile Leu Asn Leu Leu Pro Ile Thr Ser Tyr

65

70

75

80

Pro Arg Pro Gln Val Thr Trp Phe Arg Glu Gly His Lys Ile Ile Pro

85

90

95

Ser Asn Arg Ile Ala Ile Thr Leu Glu Asn Gln Leu Val Ile Leu Ala

100

105

110

Thr Thr Thr Ser Asp Ala Gly Ala Tyr Tyr Val Gln Ala Val Asn Glu

115

120

125

Lys Asn Gly Glu Asn Lys Thr Ser Pro Phe Ile His Leu Ser Ile Ala

130

135

140

Arg Asp Val Gly Thr Pro Glu Thr Met Ala Pro Thr Ile Val Val Pro

145

150

155

160

Pro Gly Asn Arg Ser Val Val Ala Gly Ser Ser Glu Thr Thr Leu Glu

165

170

175

Cys Ile Ala Ser Ala Arg Pro Val Glu Asp Leu Ser Val Thr Trp Lys

180

185

190

Arg Asn Gly Val Arg Ile Thr Ser Gly Leu His Ser Phe Gly Arg Arg

195

200

205

Leu Thr Ile Ser Asn Pro Thr Ser Ala Asp Thr Gly Pro Tyr Val Cys

210 215 220

Glu Ala Ala Leu Pro Gly Ser Ala Phe Glu Pro Ala Arg Ala Thr Ala

225 230 235 240

Phe Leu Phe Ile Ile Glu Pro Pro Tyr Phe Thr Ala Glu Pro Glu Ser

245 250 255

Arg Ile Ser Ala Glu Val Glu Glu Thr Val Asp Ile Gly Cys Gln Ala

260 265 270

Met Gly Val Pro Leu Pro Thr Leu Gln Trp Tyr Lys Asp Ala Ile Ser

275 280 285

Ile Ser Arg Leu Gln Asn Pro Arg Tyr Lys Val Leu Ala Ser Gly Gly

290 295 300

Leu Arg Ile Gln Lys Leu Arg Pro Glu Asp Ser Gly Ile Phe Gln Cys

305 310 315 320

Phe Ala Ser Asn Glu Gly Gly Glu Ile Gln Thr His Thr Tyr Leu Asp

325 330 335

Val Thr Asn Ile Ala Pro Val Phe Thr Gln Arg Pro Val Asp Thr Thr

340 345 350

Val Thr Asp Gly Met Thr Ala Ile Leu Arg Cys Glu Val Ser Gly Ala

Ser Glu Gly Gly Asn Asp Ser Arg Met Ala Arg Leu Glu Val Ile Glu

515

520

525

Leu Pro His Ser Pro Gln Asn Leu Leu Val Ser Pro Asn Ser Ser His

530

535

540

Ser His Ala Val Val Leu Ser Trp Val Arg Pro Phe Asp Gly Asn Ser

545

550

555

560

Pro Ile Leu Tyr Tyr Ile Val Glu Leu Ser Glu Asn Asn Ser Pro Trp

565

570

575

Lys Val His Leu Ser Asn Val Gly Pro Glu Met Thr Gly Val Thr Val

580

585

590

Ser Gly Leu Thr Pro Ala Arg Thr Tyr Gln Phe Arg Val Cys Ala Val

595

600

605

Asn Glu Val Gly Arg Gly Gln Tyr Ser Ala Glu Thr Ser Arg Leu Met

610

615

620

Leu Pro Glu Glu Pro Pro Ser Ala Pro Pro Lys Asn Ile Val Ala Ser

625

630

635

640

Gly Arg Thr Asn Gln Ser Ile Met Val Gln Trp Gln Pro Pro Pro Glu

645

650

655

Thr Glu His Asn Gly Val Leu Arg Gly Tyr Ile Leu Arg Tyr Arg Leu

660

665

670

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Ala Gly Leu Pro Gly Glu Tyr Gln Gln Arg Asn Ile Thr Ser Pro Glu
675 680 685

Val Asn Tyr Cys Leu Val Thr Asp Leu Ile Ile Trp Thr Gln Tyr Glu
690 695 700

Ile Gln Val Ala Ala Tyr Asn Gly Ala Gly Leu Gly Val Phe Ser Arg
705 710 715 720

Ala Val Thr Glu Tyr Thr Leu Gln Gly Val Pro Thr Ala Pro Pro Gln
725 730 735

Asn Val Gln Thr Glu Ala Val Asn Ser Thr Thr Ile Gln Phe Leu Trp
740 745 750

Asn Pro Pro Pro Gln Gln Phe Ile Asn Gly Ile Asn Gln Gly Tyr Lys
755 760 765

Leu Leu Ala Trp Pro Ala Asp Ala Pro Glu Ala Val Thr Val Val Thr
770 775 780

Ile Ala Pro Asp Phe His Gly Val His His Gly His Ile Thr Asn Leu
785 790 795 800

Lys Lys Phe Thr Ala Tyr Phe Thr Ser Val Leu Cys Phe Thr Thr Pro
805 810 815

Gly Asp Gly Pro Pro Ser Thr Pro Gln Leu Val Trp Thr Gln Glu Asp
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all other amino acids are present in the protein

820

825

830

Lys Pro Gly Ala Val Gly His Leu Ser Phe Thr Glu Ile Leu Asp Thr

835

840

845

Ser Leu Lys Val Ser Trp Gln Glu Pro Leu Glu Lys Asn Gly Ile Ile

850

855

860

Thr Gly Tyr Gln Ile Ser Trp Glu Val Tyr Gly Arg Asn Asp Ser Arg

865

870

875

880

Leu Thr His Thr Leu Asn Ser Thr Thr His Glu Tyr Lys Ile Gln Gly

885

890

895

Leu Ser Ser Leu Thr Thr Tyr Thr Ile Asp Val Ala Ala Val Thr Ala

900

905

910

Val Gly Thr Gly Leu Val Thr Ser Ser Thr Ile Ser Ser Gly Val Pro

915

920

925

Pro Asp Leu Pro Gly Ala Pro Ser Asn Leu Val Ile Ser Asn Ile Ser

930

935

940

Pro Arg Ser Ala Thr Leu Gln Phe Arg Pro Gly Tyr Asp Gly Lys Thr

945

950

955

960

Ser Ile Ser Arg Trp Ile Val Glu Gly Gln Met Arg His Gln Gly Val

965

970

975

Gly Leu Pro Ala Glu Val Thr Gln Pro Ser His Glu Ala Gly Leu Glu

980

985

990

Pro Ala Asn Leu Gly Ser Leu Trp Leu Leu Ser Leu Val Tyr Trp Cys

995

1000

1005

Tyr Ser Gln Lys Leu Trp Glu Phe Ser Cys

1010

1015

<210> 181

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Primer

<400> 181

cttctgctct aaaagctgcg

20

<210> 182

<211> 20

<212> DNA

<213> Artificial Sequence

[illegible]

1

735/735